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A1799725 pc0- Ba007
CC1601509 OB J2991
A1834106 606065A12
BF728943 1000069F0
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +>>-11-2000 Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer
This sequence was derived from the following URL
This sequence was derived from the FAPESP/LICR Human Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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CM0-NN1155-271000-628-a09
BF945949
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Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
Proc. Natl. Acad.
20202663
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TGAGAGAAATGACCACGTCGGGC
                      TGAGCGAGATGACCAGCTCCGGC 152
                                                                    GTCTGTGGCGGTAGGCTGGGTGAGGGAAAGGACCACGTCGGGCGGTAGGCTGGGTGG
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/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1155"
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Eutheria; Primates; Catarrhini; Hominidae;
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Proc. Natl. Ac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-270/uur
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Hum
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This entry can be seen in the following U
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Ludwig Touring Prudente 109, 4 and
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia; Eutheria; Primates;
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CMO-NN1155-271000-628-a09 NN1155 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                               GCCCGACGTGGTCATTTCTCTCACCACCCAGCCTACCGCCCGACGTG
                                                                                                                                                        TCGTCGAGTCGGCGGCCGAC
                                                                                                                    CCACCCÁGCCTACCGCCACAGÁC
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                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
/clone lib="NN1155"
/clone lib="NN1155"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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xref="taxon:9606"
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Catarrhini; Hominida
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ae; Homo.
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RESULT 4
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MEDLINE
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Best Local Similarity
Matches 65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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University of Iowa
375 Newton Road , 4156
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                        77
BF408161 186 bp mRNA linear IUI-R-BJ2-bra-d-05-0-UI.s1 UI-R-BJ2 Rattus norvegicus UI-R-BJ2-bra-d-05-0-UI 3', mRNA sequence.
BF408161 GI:11396136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bento-soares@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of se
is likely internal to the message. cDNA Library Preparation:
Soares Lab Clone distribution: clones will be available throu
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 1-21,
>GC_rich#Low_complexity
Seq_primer: M13 Forward
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Bonaldo,M.F., Lennon,G. and Soares
Normalization and subtraction: two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                      CGGCCTCCTGGCATGGGCCGGGGGATGAGTGTCTAGTCCGTGGCCGCTGGGCAGCCGGGG
                                                                                                                                                                                        AGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 153
                                                                                                                                                                                                                                                                                                   CGGCGGCCGGAGCTGATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATG
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UI-R-BJ2-bra-d-05-0-UI"
/lab host="DH108 (Life Technologies)"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/clone lib="UI-R-BJ2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ2 library is a subtracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15 dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
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Rodentia;
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Pred. No. 3.2e+02;
); Mismatches 54;
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on: two approaches
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Sciurognathi; Muridae;
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                                    mRNA sequence.
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IMAGE:759764
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Oligo-dT track not found, Not I site shown in begins likely internal to the message. cDNA Library Posoares Lab Clone distribution: clones will be availabearch Genetics (www.resgen.com) The following pelements were found in this cDNA sequence: 1-21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordinated Laboratory University of Iowa 375 Newton Road , 4156
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Mammalia; Eutheria;
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                                                                                                                                 AA429110
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                                                                                                                                                                                                                                                                                                                                        GGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTC
                                                                                                                                                                                                                               CCCGGCTGCCCAGCGGCCACGGACTAGACACTCATCCCCCGGCCCATGCCAGGAGGCCG 17
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aldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bra-d-05-0-UI"
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polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest.eng.uiowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
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                                                                                           127 bp mRNA
Soares total fetus Nb2HF8 9w
54 5' similar to TR:G307309 G3
                                       GI:2110653
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54.6%;
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Rodentia;
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Pred. No. 3.2e+02;
); Mismatches 54
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Sciurognathi; Murida
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                                                                                             G307309 HIS
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Preparation: M.B.
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repetitive
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ae; Murinae;
                                                                                            ens cDNA clone TONE H4. [1] ;,
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ORGANISM

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REFERENCE
AUTHORS
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AA429110/c
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AUTHORS
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Best Local S
Matches 51
                                                                                                                      ORGANISM
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        Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 127)
Hillier,L., Allen,M., Bowles,L.
Kucaba,T., Lacy,M., Le,N., Lenn
Moore,B., Schellenberg,K., Step
                                                                                                                                                                    mRNA sequence.
AA429110
AA429110.1 GI
                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                    32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                    AA429110
127 bp mRNA linear EST 16-OCT-1 zv78c11.rl Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:759764 5' similar to TR:G307309 G307309 HISTONE H4. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                      Homo
                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                GAGGAGAGCCCCAAGCCGGACAG 114
                                                                                                                                                                                                                                                                                                                                                                               AGCGAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGAGGCCGAGCTGGACAGCGAGCTCATCATCGAGTCGTGCGACGCCTCCTCCGGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:759764"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                       GI:2110653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                            Bowles, L., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31.8; DB 1;
Pred. No. 5.1e+02;
D; Mismatches 32;
            Lennon, G., Steptoe, M.,
                                                                                Craniata; Vertebrata; l
Catarrhini; Hominidae;
Marra, M., Marter, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                            Geisel, G.,
                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                         EST 16-OCT-1997
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; Homo.
                                            Jost,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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COMMENT
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AUTHORS
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ORGANISM
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VERSION
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CL176108
LOCUS
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                                                                                      TITLE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                        CL176108
CL176108.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strar
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                  1 (bases 1 to 152)

Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. GeneThresher methylation filtered genomic sequences from Sorg
                                                                                                                                                                    Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                          CL176108 152 bp DNA linear 104_382_10892902_116_31763_118 Sorghum methylatior (LibID: 104) Sorghum bicolor genomic clone 1089290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White,Y., Wylie,T., Wate
WashU-Merck EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                       bicolor
                                                                                                                                                                                                                                                                                                            sequence.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTGTCCAGCTCGGCCTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGACCAGCTCCGGCCGCCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTCCGGCTTGGGGCTCTCCTCCGAGGCCGAGGAGGCGTCGCACGA
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/lab_host="DH10B"
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db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:759764"
                                                                                                                                                                                                                                                                            GI:40688623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston,R. and Wilson,R. ject 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.8; DB 1;
Pred. No. 5.1e+02;
); Mismatches 32;
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n-filtered library
02, genomic survey
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                                                                                                                                                                                        ca; Tracheophyta; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGATGATGAGC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                    Sorghum
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Louis,

MO 63108,

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JOURNAL COMMENT
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AUTHORS
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CL176108/c
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Best Local Similarity
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                                                             source
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Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seq primer: T3 Reverse
Class: shotgun
High quality sequence stop: 152.
                                                                                              Unpublished (2004)
Contact: Bedell JA
Conton Genomics, LLC
4041 Forest Park Ave, St. Louis, M
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seq primer: T3 Reverse
Class: shotgun
High quality sequence stop: 152.
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                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 152)
Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.;
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
CL176108
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152 bp DNA linear GSS 06-JAN-2004
104 382 10892902 116 31763 118 Sorghum methylation-filtered library
(LibID: 104) Sorghum bicolor genomic clone 10892902, genomic survey
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGAC 127
                                                                              quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATX623"
                     /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/mol_type="genomic
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="Sorghum methylation-filtered library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'db_xref="taxon:4558"
'clone="10892902"
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                                                               . 152
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Pred. No. 7.2e+02;
); Mismatches 23;
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CL176109
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DEFINITION
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Best Local S
Matches 45
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les 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, M
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seq primer: Swfor Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. GeneThresher methylation filtered genomic sequences from Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Eukaryota; Viridiplantae; Liliopsida; Poales;
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                     Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bicolor
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                                                                                                                                                                                                                                                                       quality sequence stop: 152.
Location/Qualifiers
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a
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                                                                                                                  /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="10892902"
/clone_lib="Sorghum methylation-filtered
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/clone="10892902"
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Poaceae; PACCAD
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                                 128
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Orion Genomics, LLC
4041 Forest Park Ave, S
Tel: 314 615 6979
Fax: 314 615 5975
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Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W., Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J., Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A. GeneThresher methylation filtered genomic sequences from Sor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jbedell@oriongenomics.com
Plate: 382 row: e column: 22
Seq primer: SWfor Forward
Class: shotgun
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
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152 bp DNA linear GSS 06-JAN-2004

104 382 10892902 148 31762 118 Sorghum methylation-filtered library
(LibID: 104) Sorghum bicolor genomic clone 10892902, genomic survey
                                                                                                                                        Similarity 66.;
15; Conservative
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igh quality sequence stop: 152.
Location/Qualifiers
                               GATGAGCG 135
GTTGGGGG
                                                                                                     GAGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGAC 127
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/mol type="genomic DNA"
/cultivar="ATx623"
/db xref="taxon:4558"
/clone="10892902"
                                                                                                                                                                                                                             /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly—sheared, end-repaired, size fractionated to enrich for the 0.5 to 9 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
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Pred. No. 7.2e+02;
0; Mismatches 23;
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                                             CV406622 13
RCO-TN0078-310700-031-f03 T
CV406622
CV406622.1 GI:52802125
EST.
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Proc. Natl. Ac
20202663
Homo sapiens
Homo sapiens
Eukaryota; Me
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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CV406622.1
EST.
                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from
Project. http://www.ludwig.org.
                                                                                                                                                                                                                                                                                        \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
Rua Prof. Antonio Prudente 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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RC0-TN0078-310700-031-f03
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0078"
/note="Organ: testis_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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 Metazoa; Chordata; Craniata; Vertebrati
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                              (human)
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                                                                                                                                                                                                                                                                                                                                        Score 31; DB 7;
Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                       Mismatches
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TN0078 Homo sapiens
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Catarrhini; Hominida
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ae; Homo.
                                                                                                                                                                                                                                                           TGGTCCTTTCCCT 116
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 a; Euteleostomi;
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                                                                                             mRNA sequence.
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BH224923
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DEFINITION
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                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 168)
 Department of Biolo Stanford University 855 California Ave,
                                                     Maize genomic sequences Unpublished (2001) Contact: Walbot V
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survey sequence.
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BH224923.1 GI:16822338
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the
Project. http://www.ludwig.org.br.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Rese
Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                              Walbot, V.
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larity 62.0%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: testis normal; Vector: puc18; Site_1: SmaI; /note="Organ: testis normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 to 135)
                                 of Biological Sciences
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Palo Alto,
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RescueMu
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CA 94304, USA
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a; Poales; Poaceae; PACCAD
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          Stanford University

855 California Ave, Palo Alto, CA 943
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by
Reverse complemented post-ligation si
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                                                                                                                                                                                                                                                                                                                           survey sequence.
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BH224923.1 GI:16
GSS.
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Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1006122 column: 15
Class: transposon-tagged.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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1006122E07.2EL_x1
Plate: 1006122
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Unpublished (2001)
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                                                                                                                                      Department
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nilarity 60.0%;
Conservative
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu; go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."
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lab_host="DH10B"
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cultivar="mixed background
db_xref="taxon:4577"
tissue_type="leaf"
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RescueMu
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                 by 2 different sequence from
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source sequence.
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Poaceae; PACCAD
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI966631
151 bp mRNA linear EST 12-1 id57a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P
                    (brown@fas.harvard.edu)
Trace considered overall poor quality
Possible reversed clone: similarity o
                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Mel
Washington University Genome Sequencing Co
obtaining a clone please contact: Juliana
                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hirosh
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
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                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                         Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www:zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B
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/cultivar="mixed background
/db_xref="taxon:4577"
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dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:16341036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              were transformed and then screened on LB plates with illin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.6; DB Pred. No. 1e+03; O; Mismatches
  similarity on wrong now available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA"
                                                                                                                                                                                                                                                                                                                                                                   Kaestner, & Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                  Melton DNA sequencing by 
Genter For information
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                                                                                                         Brown
strand
the IMAGE consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 12-MAR-2002
                                                                                                                                                      by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58
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KEYWORDS
SOURCE
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VERSION
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BI966631/c
LOCUS
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Best Local :
                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 GATGACCAGCTCCGGCCGCC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                           1 (bases 1 to 151)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                id57a04.x1 Melton Normalized Mixed musculus cDNA clone IMAGE:5666983 3
Endocrine Pancreas Consortium
Harvard University, Howard Hughes
Dept of Molecular and Cellular Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus cDNA clone I
PII PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for clone orders contact: info@image.llnl.gov
High quality sequence stop: 1.
                                                                    Contact: Douglas Melton, Klaus H.
                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                             BI966631.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCGAGGAGGTCCGCGAGGCCCTCGCCGAGGTCGGCGTCACCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGA 99
                                                                                                                                                                                                                                                                                                                                                                              musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five libraries representing EIO.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_1:
N1-MMS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Embryonic day 10.5, E12.5, adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult islet"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:10090"
'clone="IMAGE:5666983"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                             GI:16341036
                                                                                                                                                                                                                                                                                                                                                                            (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lib="Melton Normalized Mixed Mous
                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28.8; DB 4;
Pred. No. 2.8e+03;
); Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryonic
                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                           Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      & newborn,
                                                                      Kaestner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear EST 12-MAR-2002
Mouse Pancreas 1 N1-MMS1 Mus
3' similar to TR:P94852 P94852
il Institute
7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                        & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        male
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACCGTCACCGA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pancreas 1
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REFERENCE
AUTHORS
                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
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CA002143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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Best Local S
Matches 48
                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
                                                                                                                                                               CA002143.1
EST.
                Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                              CA002143 167 bp
HS06K10r HS Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
CA002143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (brown@fas.harvard.edu)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
MGI:1953309 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGCCGAAGCCCTTGACCTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                             CCTCGCGGACCTCCTCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGAGATGACCAGCTCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: psport1; Site 1: Not 1; Site 2: Sal 1; Five libraries representing EIO.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using Superscript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
Potokina, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:5666983"
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                                                                                                                                                                                         GI:24279125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lib="Melton Normalized Mixed Mouse Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.8; DB 4;
Pred. No. 2.8e+03;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
Michalek, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GÁCGGTCAGGCCGGTGACGCCGACCTCGGCGÁGGG
                                                                                                                                                                                                                                                          wulgare
                                                                                                                                                                                                                                                                                    mRNA
Weschke, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                          linear EST 23-OCT-2002 cDNA clone HS06K10
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 Stein, N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SOURCE
ORGANISM
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CA002143/c
LOCUS
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VERSION
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                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                   JOURNAL
                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                    116 CGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                    HS06K10r HS Hordeum vulgare subsp. 5-PRIME, mRNA sequence. CA002143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graner,A.
Barley ESTs from germinating
Unpublished (2002)
Contact: Stein Nils
                                                                                                                                                                 Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                            EST.
Corrensstr. 3, 06466, Gatersleben, Tel: 039482-5522 Fax: 039482-5595
                                      Molecular Markers Group, Dep
Institute of Plant Genetics
                                                                                                                       Pooideae; Triticeae; Hordeum.

1 (bases 1 to 167)

Zhang,H., Potokina,E., Michalek,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Ml3rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 167 Std Error:
Plate: 6 row: K column: 10
                                                                                 Barley ESTs from germinating 
Unpublished (2002)
                                                                                                                                                                                                                                         CA002143.1 GI:24279125
                                                                                                                                                                                                                                                                                               CA002143
                                                                    Contact: Stein Nils
                                                                                                            Graner, A
                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGGCCTCTCCGGTGCGGCGGCGGCGCGGCGGAGGTGAGAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGC 115
                                                                                                                                                                                                                                                                                                                                                                    AGGATCCGCGGCGACGAGCTGGAGAAGACGGAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sub_species="vulgare"
/db_xref="GABI:257345"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28.8; DB 6;
Pred. No. 2.8e+03;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Std Error:
                                       Department Genbank
                                                                                                                                                                                                                                                                                              167 bp
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DEFINITION
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BF882476
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Best Local S
Matches 54
                                                                                                                                                                                       JOURNAL MEDLINE PUBMED
                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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Insert
Plate:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., dā Silva, W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.
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CM1-ET0191-051200-626-b02
BF882476
                                                                                                                                                                                                                              sequence tags
Proc. Natl. Acad.
                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF882476.1 GI:12272602
EST.
                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the
Project. This entry can be seen in
                                                                           Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCTCCGTCTCCCAGCTCGTCGCCGCGGATCCTGACGGCCCTCGGCATCTTTCTCAC 71
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Length: 167 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="HS"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of /note="Vector: pBluescript SK+; Due to a cloning cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/clone_lib="HS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="vulgare"
/db_xref="GABI:257345"
/db_xref="taxon:112509"
/clone="HS06K10"
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                                                                                                                                                                                                                                   Sci. U.S.A.
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Pred. No. 2.8e+03;
); Mismatches 42
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sapiens cDNA,
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KEYWORDS
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High quality sequence start: 24
High quality sequence stop: 180.
Location/Qualifiers
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CM1-ET0191-051200-626-b02
BF882476
BF882476.1 GI:12272602
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 180.
                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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)51200-626-b02&t3=2000-12-05&t4=1)
                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
Rua Prof: Antonio Prudente 10:
                                                                                                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. A
                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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nilarity 65.6%;
Conservative
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                     Acad.
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Pred. No. 2.8e
0; Mismatches
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No. 2.8e+03;
Lsmatches 22;
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109, 4 and
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Catarrhini; Hominida
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ae; Homo.
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AUTHORS
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EBro04_SQ001_B16_
Hordeum vulgare (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 194)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources
Unpublished (2001)
On Sep 26, 2001 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
BI777398
BI777398.2
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
Pooideae; Triticae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                          On Sep 26, 2001 this sequence version Contact: Waugh R, Marshall DF Genome Dynamics/Computational Biology Scottish Crop Research Institute Invergowrie, Dundee, DD2 5DA, Scotland Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     μ
                                                                                                                                                                                                                                                                                                                     Email: est@scri.sari.ac.uk
All sequence has a Phred quality
Seq primer: M13 reverse.
Location/Qualifiers
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                                                                                                                                               /mol type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBro04_SQ001_B16"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="ET0191"
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
/note="Organ: lung_tumor; Vector was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
/dev_stage="3 week"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
/non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
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/db_xref="taxon:9606"
/dev_stage="Adult"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                              organism="Hordeum vulgare
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Pred. No. 2.8e+03;
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k, salt-stressed, cv Optic, I
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Hordeum vulgare {
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Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Sco
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudi
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,
Development of Barley Transcriptome Resources
Unpublished (2001)
On Sep 26, 2001 this sequence version replaced gi
Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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Location/Qualifiers
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                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBro04_SQ001_B16"
/tissue_type="root"
               /dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBro04"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Note I;
/note="Vector: pSPORT1; Site_1: Sal I;
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Note I;
/note="Vector: pSPORT1; Site_1: Sal I; Site_1: Sal I;
/note="Vector: pSPORT1; Site_1: Sal I; Site_1: Sal I;
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Score 28.8; DB 4; Pred. No. 2.8e+03; 0; Mismatches 72

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Canis familiaris
Eukaryota; Metazos
Mammalia; Eutheria
1 (bases 1 to 175
                                                                                                                                                                                                                             55
                                                                                                                                       73
17:
tigr-gss-dog-17000372681097
genomic survey sequence.
CE208692
CE208692.1 GI:35364347
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1 (bases 1 to 179)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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14512627
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genomic survey sequence.
CE208692
CE208692.1 GI:35364347
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ekirknes@tigr.org
Class: shotgun.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
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/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_l: BstXI; Libraries we peripheral blood"
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Pred. No. 3.2e+03;
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dq 6
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Dog Library Canis familiaris genomic,
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CA004311
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SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 190)
                                                                                                                                                                                                                                                                                                                                          CA004311
190 bp
HS17D13r HS Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
CA004311
CA004311.1 GI:24281293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
            Email: stein@ipk-gatersleben.de
Insert Length: 190 Std Error:
Plate: 17 row: D column: 13
                                                                            Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 179)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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Canis familiaris (dog)
Canis familiaris
                                                                                                                                                            Barley ESTs from germinating Unpublished (2002)
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Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, J.C.
The dog genome: survey sequencing and comparative Science 301 (5641), 1898-1903 (2003)
                                                               Fax: 039482-5595
                                                                                                                                               Contact: Stein Nils
                                                                                                                                                                                                             Zhang, H., Potokina, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-0200
Fax: 301-838-0208
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llarity 57.1%;
Conservative
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were
peripheral blood"
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Ml3rev
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Pred. No. 3.2e+03;
); Mismatches 39
                                                                                                                                                                                                             Michalek, W.,
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Genomics,
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RESULT 26
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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HS17D13r HS Hordeum vulgare
5-PRIME, mRNA sequence.
CA004311
CA004311.1 GI:24281293
                                                                                                                                                                                                                                                                                                                  Email: stein@ipk-gatersleben.de
Insert Length: 190 Std Error:
Plate: 17 row: D column: 13
Seg primer: M13rev.
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Institute of Plant Genetics and Crop Plant Research
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
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Barley ESTs from germinating seeds
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Stein Nils
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/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/clone_lib="HS"
/clone_lib="XL10-Gold"
/clone_li
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db_xref="GABI:259529"
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cultivar="barke"
sub_species="vulgare"
/db_xref="GABI:259529"
/db_xref="taxon:112509"
/clone="HS17D13"
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'clone="HS17D13"
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                                                                                                                                          mol_type="mRNA"
cultivar="barke"
                                                                                                                                                                                                               organism="Hordeum vulgare
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Best Local S
Matches 51
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1 (bases 1 to 147)

1 (bases 1 to 147)

Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN423515
17000600057518 GRN_PREHEP
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CN423515.1 GI:47411109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 650 473 8658 Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 Constitution Drive, Menlo
                                                                                                                                               Similarity
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                                                         CGCGTCGGATTCGGCCATCTCCACGCGCGGCGAGAGGTC
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/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
/clone_lib="HS"
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/clone_lib="XL10-Gold"
/clone_lib="ALL10-Gold"
/clone
                                                                                                                      Conservative
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/note="oligo dT primed, full-length
from DMSO-treated hES cell line H9 (
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic
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Pred. No. 3.2e+03;
0; Mismatches 44;
                                                                                                               Score 28.2; DB 7;
Pred. No. 4e+03;
); Mismatches 38;
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cDNA 5', mRNA sequence.
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                                                                                                                                                                         Length
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                                                                                                                   0; Gaps
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CN423515/c
                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.3%;
Best Local Similarity 57.3%;
Matches 51; Conservative
                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                         124
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (bases 1 to 196)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute / National Institute of N
                                                                                                                                                                                              tn37c01.x1 NCI_CGAP_Brn25
                                                                                           Homo sapiens
                                                                                                                                 AI564785.1
EST.
                                                                                                                                                                   mRNA sequence
AI564785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geron Corporation
230 Constitution Drive, Menlo
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                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fi
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
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17000600057518 GRN_PREHEP
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CN423515.1 GI:47411109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rbrandenberger@geron.com
Length: 147 Std Error: 0.00.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GRN_PREHEP"
/note="oligo dT_primed, full-length
from DMSO-treated hES cell line H9 (
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="embryonic stem cells, DMSO-treated
                                                                                                                                                 GI:4523242
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28.2; DB 7; L
Pred. No. 4e+03;
""" "matches 38;
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15', mRNA sequence
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                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
Mammalia; Eutheria; Primates; Catarrhini; Hominida
1 (bases 1 to 196)
1 (bases 1 to 196)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute / National Institute of I
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 277 Std Error: 0.00
Seq primer: -40UP from Gibco
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tn37c01.x1 NCI_CGAP_Brn25
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Ph.D.
                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                      Disorders and Stroke, Brain Tumor (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                       mRNA sequence.
AI564785
                            Tissue Procurement:
CDNA Library Preparation: M.
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llarity 57.3%;
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/db_xref="taxon:9606"
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Pred. No. 4e+0
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Bento
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Hominidae; Homo.
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IMAGE:2169792 3',
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                           Rosenfeld M.D.,
M. Fatima
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AI799725
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TITLE
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Best Local Similarity
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                        Bonaldo, Ph.D.

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

DNA Sequencing by: Washington University Genome

Clone distribution: NCI-CGAP clone distribution

Clone distribution: NCI-CGAP clone distribution
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1 (bases 1 to 196)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

DNA Sequencing by: Washington University Genome

Clone distribution: NCI-CGAP clone distribution

Clone distribution: M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
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mRNA sequence.
AI799725
found through the I.M.A.G.E. Consortiu www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco.
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 277 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens (human)
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Ph
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mol_type="mRNA"

db_xref="taxon:9606"

clone="IMAGE:2169792"
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Homo sapiens cDNA clone IMAGE:2164435 3',
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AI799725/c
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Ne Disorders and Stroke, Brain Tumor Genome Anatomy Pro (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. R
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cDNA Library Arrayed by: Greg Lennon,
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Phage of the property 
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/db_xref="taxon:9606"
/clone="IMAGE:2164435"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2164435"
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ae; Homo.
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          Pharmacia) with a 2: Eco RI; 1st
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IMAGE:2164435 3',
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Kim, H., Yu, Y., Stum F

Kudrna, D
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OB Ba0070005 3', ge
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GSS.
Oryza brachyantha
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                           . Similarity 63; Conserv
                                                                                                                                                                                                                                                                                  FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0070 row: O column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
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Unpublished (2004)
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CGGCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
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                                              Conservative
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                                                                                                                   /dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OB__Ba"
/note="Vector: pAGIBAC1;
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                            tissue_type="leaves"
                                                                                                                                                                                           /organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
/clone="OB_Ba0070005"
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                                                          18.3%;
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B_Ba Oryza brachyantha genomic
genomic survey sequence.
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Pred. No. 4e+0
0; Mismatches
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Pred. No. 4e+0:
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4e+03;
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4e+03;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 197)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: TAA TAC GAC TCA CTA TAG BACKWARD: CAC TCA TTA GGC ACC CCA Insert Length: 145000 Std Error Plate: 0070 row: O column: 05 Seg primer: CAC TCA TTA GGC ACC Class: BAC ends.
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Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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Arizona Genomics Institute
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Kudrna,D., Muller,C., Ha
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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_Ba0070005 3', genomic survey sequence.
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ilarity 52.1%;
Conservative
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/note="Vector: pAGIBAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
/clone="OB_Ba0070005"
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Pred. No. 4e
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RESULT 36
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BF760525.1 GI:12108425
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2&t2=RC2-CT0652-
211200-011-b01&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/dev_stage="Adult"
/clone_lib="CT0652"
/note="Organ: colon; Vector: pucl8; Site_1: SmaI; Site_2:
/mote="Organ: colon; Site_1: SmaI; Site_2: SmaI; SmaI; Site_2: SmaI; Site_2: SmaI; Site_2: SmaI; SmaI; Site_2: SmaI; Sm
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"" amatches 25;
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CT0652 Homo sapiens cDNA,
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC2&t2=RC2-CT0652-
211200-011-b01&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 130.
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Ludwig Institute for Cancer Research
Ludwig France Prudente 109, 4 andar, 01509-010,
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                   Zea mays
                                                                          CB251950.1
EST.
Eukaryota; Viri
Spermatophyta;
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Fax: +55-11-2707001
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Proc. Natl. Acad.
20202663
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Mammalia; Eutheria;
                                                       Zea mays
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                                                                                                                           19_1_H10.y_1
ea mays cDNA,
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/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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rta; Magnoliophyta; Liliopsida; Poales;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28;
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  ta; Tracheophyta;
Poaceae; PACCAD
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Stanford University
855 California Ave, Palo Alto, CA 9
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
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Location/Qualifiers
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                                                                                                                                                                     Stanford University
855 California Ave, Palo Alto,
Tel: 650 723 2227
Fax: 650 725 8221
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Maize ESTs from various cDNA libraries
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                                                                                                                                                                                                                                                                                       Department of Biological Sciences
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                                                                             walbot@stanford.edu
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'lab_host="E. col
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cultivar="B73"
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organism="Zea mays"
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Pred. No. 5.1e+03;
D; Mismatches 37;
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and Hake
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606065A12.x1 606 - Ear tissue
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Similarity 57.5%;
50; Conservative
                                                                                                                                                                                                                                                                                                                          855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Plate: 606065 row: A column:
Location/Qualifiers
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Department of Biological Sciences
Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Maize ESTs from various
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                                          Conservative
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/dev_stage="2 mm"
/lab_host="E. coli 2
/clone_lib="3529 - 3
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EcoRI; Site_2: l
Schmidt lab"
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                                                                                                                                                                                                                               organism="Zea mays"
(mol_type="mRNA"
(cultivar="Ohio43"
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/tissue_type="mixed"
/dev_stage="ear length from 0.5
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDN
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                                         Score 27.8; DB 1
Pred. No. 5e+03;
0; Mismatches 3
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Pred. No. 5.1e+03;
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                                            37;
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Poaceae; PACCAD
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chmidt lab Zea
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606065A12.x1 606 ·
mays cDNA, mRNA so
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: walbot@stanford.edu
Plate: 606065 row: A column:
Location/Qualifiers
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               Zea mays
                           Zea mays
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: 650 723 2227
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EcoRI; Site_2:
Schmidt lab"
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/tissue_type="mixed"
/dev_stage="ear length from 0.5 cm
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA l
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(mol_type="mRNA"
(cultivar="Ohio43"
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                               sequence.
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Unigene
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Pred. No. 5e+03;
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                                                       Contact: Walbot V
Department of Biological S
Stanford University
855 California Ave, Palo A
Tel: 650 723 2227
Fax: 650 725 8221
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Stanford University
855 California Ave, Palo A
Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophy Spermatophyta; Magnoliophyta; Liliopsida; Poales; clade; Panicoideae; Andropogoneae; Zea.
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Plate: 1000069 row: F column:
Location/Qualifiers
            Email: walbot@stanford.edu
Plate: 1000069 row: F colu
Location/Qualifiers
                                                                                                                                                   University
Unpublished (1999)
                                                                                                                                                                                               Walbot, V
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Contact: Walbot V
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Maize ESTs from
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/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets wer
also selected."
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/db_xref="dbEST:945002F06.X3"
/db_xref="taxon:4577"
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No. 5e+03;
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Poaceae; PACCAD
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AUTHORS
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AJ469411
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Matches 44
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Best Local Similarity 57.5%;
Matches 50; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 180)
Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                    46
                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
Contact: Schulman AH
Institute of Biotechnology
University of Helsinki
P.O.Box 56 (Viikinkaari 6A),
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                                  GCCGGCCGACGCCCCCCCCGCGGAGGAGGACGACGCCATCACCATCAAGGGCGTGCG
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/note="This library represents the unique ESTs found in
/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets wer
also selected."
                                                                                                                                                                                      /organism="Hordeum vulgare"
/mol_type="mRNA"
/db_xref="taxon:4513"
/clone="S0000800047F11F1"
/tissue_type="Callus"
/clone_lib="S00008"
/note="Callus K19"
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/mol_type="mRNA"
/db_xref="dbEST:945002F06.X3"
/db_xref="taxon:4577"
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Pred. No. 5e+03;
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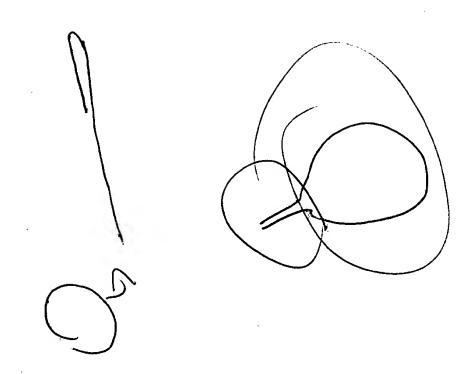
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RESULT 44
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Best Local Similarity
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JOURNAL
       Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Seque
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, 1
Tel: 516 367 8884
Fax: 516 367 8874
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; l
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 180)
Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman,
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ig24e03.bl WGS-ZmaysF (DH5a methyl
ig24e03, genomic survey sequence.
CC157563
CC157563.1 GI:30182343
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University of Helsinki
P.O.Box 56 (Viikinkaari 6A
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Contact: Schulman
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1 (bases 1 to 184)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., D. Ratzenburger, F., King, L., Miller, B., Muller, S., N. Zutavern, T., McCombie, W.R. and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-free; Liber, 1900)
                                                                                                                                                                                                                                         Zea mays
Email: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACTCGACGATGAGCGAGATGACCAGC
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nilarity 57.5%;
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/db xref="taxon:4513"
/clone="S0000800047F11F1"
/tissue type="Callus"
/clone_lib="S00008"
/note="Callus K19"
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mol_type="mRNA"
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Pred. No. 5e+03;
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Poaceae; PACCAD
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Search completed: April 9, 2005, 02:31:57 Job time : 3011 secs
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Class: shotgun
High quality sequence stop: 184.
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ig24e03"
/clone="ig24e03"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/clone="ig24e03"
/clone="ig24e0
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: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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IS-09-934-900-25
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IS-10-981-293-25
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Sequence 24, Appl Sequence 24, Appl Sequence 14, Appl Sequence 158821, Sequence 158821, Sequence 31230, A Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 21853, A Sequence 21853, A Sequence 21754, A Sequence 21754, A Sequence 4668, Apsequence 25686, Apsequence 25686, Apsequence 15, Appl Sequence 25686, Apsequence 26669, Apsequence 140476, Sequence 28, Appl Sequence 28, Appl Sequence 15, Appl Sequence 140476, Sequence 28, Appl Sequence 15, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 27, Appl Sequence 162391, Sequence 2476, Apsequence 162391, Sequence 162391, Sequence 27978, A Sequence 27978, A Sequence 162391, Sequence 162391, Sequence 162391, Sequence 162391, Sequence 17, Appli Sequence 17, Appli Sequence 162391, Sequence 162391, Sequence 162391, Sequence 17, Appli Sequence
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RESULT 1

US-09-887-194A-13

Sequence 13, Application US/09887194A

Publication No. US20030036197A1

GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Nichols, Scott E.
CURRENT FILING DIAMA

CURRENT FILING DIAMA

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO 13

LENGTH: 154

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION. Description of Artificial
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US-09-887-194A-13/c
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Sequence 13, Application US/09887194A Publication No. US20030036197A1 GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F. APPLICANT: Gordon-Kamm, William J. APPLICANT: Kinney, Anthony APPLICANT: Lowe, Keith S.
                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 154; Conservative (
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US-10-741-601-3022
US-10-741-601-3022
US-10-741-601-3115
US-10-741-601-3115
US-10-741-600-11671
US-10-741-600-11762
US-10-741-600-11762
US-10-741-600-11855
US-10-425-115-3104
US-10-425-115-3104
US-10-424-599-56083
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Pred. No. 2.2e-37;
Mismatches 0;
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; OTHER INFORMATION: Des
; OTHER INFORMATION: reg
US-09-887-194A-13
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APPLICANT: Stecca, Kevin L.
FITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 154
TYPE- DNA
                                                                                                                                                                                                                                                                  APPLICANT: Yadav, Naren
ITITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
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APPLICANT: Booth, Ru
APPLICANT: Cahoon,
APPLICANT: Hitz, Wi
APPLICANT: Kinney,
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Best Local Similarity
Matches 154; Conserv
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial
FEATURE:
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Hitz, William D
Kinney, Anthony
Yadav, Naren
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                         CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
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No. US20030054521A1
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Pred. No. 2.2e-37;
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CURRENT APPLICATION NUMBER: US/09/934, CURRENT FILING DATE: 2001-08-22; PRIOR APPLICATION NUMBER: 60/226996; PRIOR FILING DATE: 2000-08-22; NUMBER OF SEQ ID NOS: 26; SOFTWARE: Microsoft Office 97; SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-734-947-7
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                                                                        TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO CTITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES FILE REFERENCE: BB1535 US NA CURRENT APPLICATION NUMBER: US/10/734,947 CURRENT FILING DATE: 2003-12-11 PRIOR APPLICATION NUMBER: US 60/433,433 PRIOR FILING DATE: 2002-12-13 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Microsoft Office 97 SEQ ID NO 7 LENGTH: 154
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10734947 Publication No. US20040128714A1
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APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
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ORGANISM: Artificial
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                                     ORGANISM: Artificial Sequence
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No. US20030054521A1
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Artificial sequence containing
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RESULT 7
US-10-981-293-25
; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
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                                                                 APPLICANT: Booth, Russ APPLICANT: Cahoon, Rel
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OTHER INFORMATION:
US-10-981-293-25
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                                                                Query Match
Best Local S
Matches 154
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                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
TYPE: DNA
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CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/22696
PRIOR APPLICATION NUMBER: 60/22696
PRIOR FILING DATE: 2000-08-22
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TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Office 97
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LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                  OTHER INFORMATION: Description of Artificial OTHER INFORMATION: region of pKS133
                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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54; Conservative
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Yadav, Naren
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Hitz, William D
                                                                  Conservative
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                                                               100.0%; Score 154; DB 19; 100.0%; Pred. No. 2.2e-37; ive 0; Mismatches 0;
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                                 CGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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US-09-887-194A-12/c
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                                                                                                               APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
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SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Glassman,
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Best Local
                                               SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: region of pKS106 and pKS124
 OTHER INFORMATION:
                                 FEATURE:
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Gordon-Kamm, William G
Kinney, Anthony
Lowe, Keith S.
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Vo. US20030036197A1
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Description of Artificial Sequence: region of pKS106 and pKS124
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RESULT 12
US-09-934-900-24/c
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
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US-09-934-900-24
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APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
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APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 24
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: region of pKS106 and pKS124
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Hitz, William D
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Hitz, William D
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100.0%; Pred. No. 6.3e-15;
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RESULT 14
US-10-981-293-24/c
; Sequence 24, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
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US-10-981-293-24
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LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No.
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SOPTWARE: Microsoft Office
SEQ ID NO 24
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APPLICANT:
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SOFTWARE: Microsoft Office
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APPLICANT: Cahoor
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ORGANISM: Artificial
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APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ANI
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 92
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                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09887194A Publication No. US20030036197A1 GENERAL INFORMATION:
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                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Glassman, Kimberly F. APPLICANT: Gordon-Kamm, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: BB1476 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleotide Sequences of TITLE OF INVENTION: ACP Desaturase
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                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                          FEATURE:
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                                                                                                                       Local
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                                                                                                                      Similarity
                          GAGATGACCAGCTCCGGCCG 117
                                                                             GAGATGACCAGCTCCGGCCG 117
                                                   CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGACTCGACGATGAGC
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Lowe, Keith S.
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Hitz, William D
                                                                                                          Conservative
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ID NOS: 26
                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: region of pKS106 and pKS124
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                                                                                                                    100.0%;
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                                                                                                        Score 80; DB; Pred: No. 6.2
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86
                                                                                                                                                                         of Artificial Sequence:
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. 6.3e-15;
                                                                                                                     DB 10; I
6.2e-15;
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APPLICANT: Lowe, Keith S.

APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND FILE REFERENCE: BB1449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A;

CURRENT FILING DATE: 2002-03-13;

NUMBER OF SEQ ID NOS: 36;

SOFTWARE: Microsoft Office 97;

SEQ ID NO 14
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; OTHER INFORMATION:
US-10-425-115-158821
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                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 158821 LENGTH: 191
                                                                                                              Matches
                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 158821, Application US/10425115 Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09887194A Publication No. US20030036197A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 92
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                            Local Similarity
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                                                                          GCTCATCGTCGAGTCGGCGGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCG 80
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Zhou, Yihua
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                                                                                                             Conservative
                                                                                                                                                                                   Clone ID: MRT4577_76420C.
                                                                                                                         18.4%;
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                                                                                                           Score 28.4; Di
Pred. No. 27;
O; Mismatches
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6.2e-15;
hes 0;
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                                                                                                        Indels
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                                                                                                         0; Gaps 0;
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CCATCACGGTGCTGTAGGAGATGCTGGATGCCGTCCGCCTACAGGACGACGACGACGCGA 134

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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asscrittle OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 158821

LENGTH: 191

TYPE: DW"
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US-10-425-115-158821/c
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                                                                                                                          US-10-437-963-9894
                                                                                                                                                                                                    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 9894

LENGTH: 175
                                                           Best Local Matches '
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                                                                                                                                                TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
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OTHER INFORMATION: Clone ID:
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                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT4530_16268C.1
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.ication No. US20040123343A1
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Zhou, ri...
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Kovalic, David
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                              Boukharov, Andrey A.
Barbazuk, Brad
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Zhou, Yihua
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                                                           Score 27.4; D
Pred. No. 54;
0; Mismatches
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Pred. No. 27;
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SEQ ID NO 9894
LENGTH: 175
                                                            NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 31230
LENGTH: 195
                                                                                                                                                                                                                                                                                                                             Sequence 31230, Application US/10437963 Publication No. US20040123343A1
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                                                                                                                                                                                                                                                                                               GENERAL INFO APPLICANT:
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                                                                                                        APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other
TITLE OF INVENTION: Plants and Uses Thereof for Plant Imp
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other TITLE OF INVENTION: Plants and Uses Thereof for Plant Imperite Reference: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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OTHER INFORMATION: Clone ID: PAT_MRT4530_16268C.1
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              FEATURE:
                              TYPE: DNA
ORGANISM: Oryza
  OTHER INFORMATION: Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 62.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTCGACG 91
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                                                                                                                                                                                                                                        Zhou, III....
Tan. Yongwei
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Barbazuk, Brad
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Zhou, Yihua
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ID: PAT_MRT4530_35558C.1
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Pred. No. 54
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EARLIER FILING DATE: 1998-01-14

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APPLICANT: ROBELL,
APPLICANT: Liu, Rihe
APPLICANT: Liu, Rihe
ITITLE OF INVENTION: SELECTION OF PROTEINS USING KEYL
ITITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/09/876,235
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
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US-09-876-235-34
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US-10-437-963-31230/c
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 31230
LENGTH: 195
TYPE: DNA
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Best Local Similarity 54.1%;
Matches 53; Conservative
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Publication No. US20040123343A1
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APPLICANT: Roberts, Richar
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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Cao, Yongwei
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Barbazuk, Brad
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Pred. No. 1.4e
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Pred. No. 1.4e+02
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1.4e+02;
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APPLICANT: Liu, Rihe

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTE

CURRENT OF INVENTION: FUSIONS

FILE REPERENCE: 00786/350005

CURRENT APPLICATION NUMBER: US/09/876,235

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/PRIOR FILING DATE: 1999-02-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FASTSEQ for Windows Version 4.0
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; OTHER INFORMATION:
US-09-876-235-34
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US-09-876-235-34/c
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; OTHER INFORMATION: n
US-09-876-235-34
                                                                                                         Query Match
Best Local Similarity 15.0
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Publication No.
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Best Local (
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TYPE: DNA
ORGANISM: Homo s
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                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo
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                            GATGAGCGAGATGACCAGCTCCGGCCGACTCGACGATGAGCGAG
                                                           CCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTC
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RESULT 25 US-10-764-799-34

Sequence 34, Appublication No

Application US/10764799

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Szostak, Jack W. Roberts, Richard

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; OTHER INFORMATION: n =
US-10-764-799-34
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                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/764,799
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
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CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
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                 Query Match
Best Local
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Best Local :
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TITLE OF INVENTION: SELECTION OF
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350005
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richar
                                                                                                                                                                                SOFTWARE:
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                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                 ) ID NO 34
ENGTH: 123
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 Score 25; DB Pred. No. 2.9e
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Pred. No.
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                              Length 123;
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RESULT 28
US-10-029-386-21853/c
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US-10-029-386-21853
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                                                                                                                                  SOFTWARE: Annomax Sequence SEQ ID NO 21853
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Best Local
                                                                                                                                                                    APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED :
TITLE OF INVENTION: EXPRESSION ANALYSIS :
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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TITLE OF INVENTION: HUMAN GENOME-DERIVED |
TITLE OF INVENTION: EXPRESSION ANALYSIS |
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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                                                                                                                                                                                                                                                                                                          APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8

OTHER INFORMATION: MT HIT: AF166267.1, EVALUE 2.00e-08

OTHER INFORMATION: EST_HUMAN HIT: BG122566.1, EVALUE 4.00e
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 OTHER INFORMATION:
OTHER INFORMATION:
                                                                        TYPE: DNA
ORGANISM: Homo
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                                                         FEATURE:
                                                                                                                  ENGTH:
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MAP TO CHR19.
EXPRESSED IN EXPRESSED IN
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72.7%;
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                                                                                                                                                   Listing Engine
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Pred. No. 3.4e+02;
); Mismatches 12
BRAIN, SIGNAL
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NO 21754
LENGTH: 167
TYPE: TYPE:
                                  APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION UNMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 21754
LENGTH: 167
TYPE: DNA
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  US-10-7
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Best Local S
Matches 32
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Best Local (
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OTHER INFORMATION: Clone .0-767-701-21754
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                           FEATURE:
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Similarity 57.0%;
45; Conservative
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EXPRESSED IN LUNG, SIGNAL = 3.5
EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
NT HIT: AF166267.1, EVALUE 2.00e-08
SWISSPROT HIT: Q05090, EVALUE 3.00e-03
EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
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Pred. No. 3.8e+02;
0; Mismatches 34;
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Pred. No. 3.4e+02;
D; Mismatches 12
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; Sequence 4668, Application U; Patent No. US20020013958A1; GENERAL INFORMATION: ; APPLICANT: Lalgudi, Raghuna; APPLICANT: Kamigaki, Laura APPLICANT: Sherman, Bradle;
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US-09-923-876-4668
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION UMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PERL Program
SEQ ID NO 4668
LENGTH: 164
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte II
NAME/KEY: unsure
LOCATION: 150
OTHER INFORMATION: a, t, c,
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Best Local
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR APPLICATION NUMBER: 60/085,331
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nilarity 60.6%;
Conservative (
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i, Laura Y. (Ito)
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Pred. No. 3.8e+02;
0; Mismatches 34;
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Pred. No. 4.4e
O; Mismatches
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4.4e+02;
ches 26;
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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyt
; NAME/KEY: unsure
; LOCATION: 150
; OTHER INFORMATION: a, t,
US-09-923-876-4668
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; OTHER INFORMATION: Incyt
; NAME/KEY: unsure
; LOCATION: 150
; OTHER INFORMATION: a, t,
US-09-923-876-4668
RESULT 34
US-09-923-876-4668/c
e-muence 4668, Application US/09923876
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US-09-923-876-4668
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Best Local Similarity 60.6
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SEQ ID NO 4668
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ORGANISM: Zea mays
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Pred. No. 4.4e+02;
0; Mismatches 26;
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Pred. No. 4.4e+02;
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APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 62701

LENGTH: 183

TYPE: rw*
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                                                                                                                                      Query Match
Best Local
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SOFTWARE: PERL Program
SEQ ID NO 4668
                                                                                                                      Matches
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NAME/KEY: misc feature
OTHER INFORMATION: Incyt
NAME/KEY: unsure
LOCATION: 150
OTHER INFORMATION: a, t,
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                 y Match 15.8%;
Local Similarity 56.1%;
nes 46; Conservative
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107 AGCTCCGGCCGCCGACTCGACG 128
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                                                    CGGATCACCTGGCTCAGCGGCGAGGCCGAGGGCAACGGCCCACGCAA
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                                                                                   CTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACC 106
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                                                                                                                   Score 24.4; DB 18;
Pred. No. 4.4e+02;
); Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.4; DB 10
Pred. No. 4.4e+02;
); Mismatches 26
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                                                    derecredidese 78
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US-09-864-761-25686
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US-10-425-115-62701/c
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                                                                                                                            CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 62701
LENGTH: 183
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Best Local
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PRIOR
PRIOR
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE I
  PRIOR
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
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. US20020048763A1
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Zhou, Yihua
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RESULT 38
US-09-864-761-25686/c
; Sequence 25686, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE INTITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY FILE REFERENCE: Aeomica-X-1 CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron
APPLICANT: Rank, David F
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OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
OR APPLICATION NUMBER: US 09/608,408
OR FILING DATE: 2000-06-30
OR APPLICATION NUMBER: US 09/774,203
OR FILING DATE: 2001-01-29
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HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6

HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13

HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4

HER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.6

HER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15

HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.7

HER INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 6.7

HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6

HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6

HER INFORMATION: SWISSPROT HIT: P30046, EVALUE 1.00e-100

HER INFORMATION: EXILABINATION: EXPRESSED IN HELA, SIGNAL = 8.6

HER INFORMATION: SWISSPROT HIT: P30046, EVALUE 1.00e-28

HER INFORMATION: EST_HUMAN HIT: AV655183.1, EVALUE 1.00e-10
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TH: 185
APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
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APPLICATION NUMBER: PCT/US01/00670
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Hanzel, David K.
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RESULT 39
US-10-753-646-15
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
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ORGANISM: Homo
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OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00668
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR APPLICATION NUMBER: PCT/US01/00661
OR APPLICATION NUMBER: PCT/US01/00661
OR APPLICATION NUMBER: PCT/US01/00670
OR APPLICATION NUMBER: DCT/US01/00670
OR APPLICATION NUMBER: US 60/234,687
OR APPLICATION NUMBER: US 69/608,408
OR APPLICATION NUMBER: US 09/774,203
OR APPLICATION NUMBER: US 09/774,203
OR APPLICATION NUMBER: US 09/774,203
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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N: EXPRESSED IN LUNG, SIGNAL = 8.6

N: EXPRESSED IN ADULT LIVER, SIGNAL = 13

N: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4

N: EXPRESSED IN PLACENTA, SIGNAL = 7.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 15

N: EXPRESSED IN HEART, SIGNAL = 5.6

N: EXPRESSED IN HEART, SIGNAL = 6.7

N: EXPRESSED IN HEART, SIGNAL = 8.6

N: EXPRESSED IN HELA, SIGNAL = 8.6

N: EXPRESSED IN HELA, SIGNAL = 8.6

N: EXPRESSED IN HELA, SIGNAL = 8.6

N: SWISSPROT HIT: P30046, EVALUE 1.00e-100

N: SWISSPROT HIT: AV655183.1, EVALUE 1.00e-100
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Pred. No. 4.4e+02;
D; Mismatches 61;
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APPLICANT: DAVIdSON, DONAID J.

FITTLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,

FITTLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND

FILE REFERENCE: 5940.US.P3

CURRENT APPLICATION NUMBER: US/10/753,646

CURRENT FILING DATE: 2004-01-08

PRIOR APPLICATION NUMBER: US/08/924,287A

PRIOR FILING DATE: 2004-01-08

PRIOR APPLICATION NUMBER: US 08/851,350

PRIOR APPLICATION NUMBER: US 08/851,350

PRIOR APPLICATION NUMBER: US 08/832,087

PRIOR FILING DATE: 1997-04-03

PRIOR FILING DATE: 1996-05-03

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-753-646-15/c
                                                              ; OTHER INFORMATION: US-10-753-646-15
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CURRENT FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US/08/924,287A
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: US 08/851,350
PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR APPLICATION NUMBER: US 08/643,219
PRIOR APPLICATION NUMBER: US 08/643,219
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Davidson, Donald J
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Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows
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TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING SAME
TITLE OF INVENTION: ANGIOGENESIS
FILE REFERENCE: 5940.US.P3
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                                                                                                                                                LENGTH: 17
TYPE: DNA
                                                                                                                             ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 CATCACGGTGGTGGTCTGGTGCCGCGCGCAGCTGAAGAGCTGGCTC
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No. US20040138127A1
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                                                                                    Synthetic
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                                                                                    DNA Fragment
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Score
Pred.
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Pred. No. 5.1e+02;
D; Mismatches 23;
 24.2;
No. 5.
 DB 18;
.1e+02;
                                                                                   synVB2
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                      175;
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 140476
LENGTH: 183
TYPE: DN"
                                                                 APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules & TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 140476

LENGTH: 183
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US-10-425-115-140476
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; OTHER INFORMATION:
US-10-425-115-140476
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                            GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (1)..(183)
OTHER INFORMATION: un
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ORGANISM: Zea mays
 FEATURE:
NAME/KEY:
LOCATION:
                                          TYPE: DNA
ORGANISM: Zea mays
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(1)..(183)
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56.4%;
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Pred. No. 5e+02;
0; Mismatches 34;
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OTHER INFORMATION: Clone ID: US-10-425-115-140476
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; LOCATION: (1)..(192)
US-10-156-761-3130
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US-10-156-761-3130/c
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APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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SEQ ID NO 3130
LENGTH: 192
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Best Local (
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Best Local Similarity 64.8%;
Matches 35; Conservative
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
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ORGANISM: Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 TCGGGTTCTATCTCGCGTCCTCGACCGTCGCCCGACCATCAACGAG
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Similarity 56.4%;
44; Conservative
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Pred. No. 5e+02;
0; Mismatches 34;
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Pred. No. 7.7e+02;
D; Mismatches 19;
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3130
LENGTH: 192
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(192)
US-10-156-761-3130
Search completed: April
Job time : 498 secs
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US-10-425-115-22757
; Sequence 22757, Application US/10425115; Publication No. US20040214272A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 22757
LENGTH: 155
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                      Query Match 15.2%; Score 23.4; DB 18; Best Local Similarity 50.0%; Pred. No. 8.9e+02; Matches 42; Conservative 0; Mismatches 42;
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Best Local Similarity 64.8%;
Matches 35; Conservative (
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NAME/KEY: unsure
LOCATION: (1)..(155)
OTHER INFORMATION: unsure at all n locations
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Pred. No. 7.7e+02;
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JS-08-952-670-3
JS-08-952-670-3
JS-08-952-670-3
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JS-09-513-999C-16612
JS-08-851-350-15
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SOFTWARE: PERL Program
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TITLE OF INVENTION: POLYNUCLEOTIDES AND PORTION REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                   APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                                      FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
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LOCATION: 108, 196
OTHER INFORMATION: a, t,
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NAME/KEY: misc_feature
OTHER INFORMATION: Inc
                                        NAME/KEY: misc_feature
OTHER INFORMATION: Inc;
NAME/KEY: unsure
                                                                                                       TYPE: DNA
ORGANISM: Zea mays
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                                                                                             FEATURE:
OCATION: 108, 196
THER INFORMATION:
-313-294A-6653
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ANT: Lalgudi, Raghunath
ANT: Ito, Laura Y.
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Similarity 51.2%;
64; Conservative
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RESULT 4
US-09-513-999C-13979/c
; Sequence 13979, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
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US-09-513-999C-13979
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Best Local Similarity
Matches 64; Conserv
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded
Patent No. 6783961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13979
LENGTH: 195
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                                                                                                                                                                                                                                                                            Query Match
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 57
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n=a,
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OTHER INFORMATION: 8=9
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Pred. No. 2e+02;
0; Mismatches 6
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Pred. No. 4.5e+02;
D; Mismatches 39;
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APPLICANT:

J.Y.

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RESULT 5
US-09-621-976-19276
; Sequence 19276, Application US/09621976
parent No. 6639063
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SOFTWARE: Patent.pm
SEQ ID NO 13979
                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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LOCATION: 11
OTHER INFORMATION: n=a,
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OTHER INFORMATION: 8=9
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NAME/KEY: misc_feature
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                           CGAGATGACCAGCTCCGGCCGCCGACTCG 125
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                                                                                                                 Score 26.2; DB 4;
Pred. No. 5.7e+02;
Nismatches 39;
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Pred. No. 4.5e+02;
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                                                                                                                                             Length 171;
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US-09-621-976-19276/c
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 19276
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,670
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00821
FILING DATE: 31-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06578
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REPERENCE/DOCKET NUMBER: 065691/0128
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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APPLICANT: Aufrere,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                      ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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3000 K Street,
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Pred. No. 5.7e+02
L; Mismatches 3
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US-08-952-670-3
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Best Local (
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                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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SEQUENCE C
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                                                                                                                    REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00821
FILING DATE: 31-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06578
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,670
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                               NAME: Granados, Pat REGISTRATION NUMBER:
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TOPOLOGY: 1
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E CHARACTERISTICS:
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(genomic)
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US-09-247-190-34
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/09/247,190
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
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Best Local (
                                           TITLE OF INVENTION: SELECTION OF PROTEINS TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350005 CURRENT APPLICATION NUMBER: US/09/247,190 CURRENT FILING DATE: 1999-02-09 EARLIER APPLICATION UMBER: 00/035,963 EARLIER FILING DATE: 1997-01-21 CARLIER ADDITION NUMBER: 60/06/461
                                                                                                                                                                                                                                                                            APPLICANT: Szostak, APPLICANT: Roberts, APPLICANT: Liu, Rih
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SOFTWARE: FastSEQ for Windows Version
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FILING DATE: 1997-01-21
APPLICATION NUMBER: 60/064,491
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US-09-513-999C-16612/c; Sequence 16612, Appl: Patent No. 6783961; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Versey ID NO 34
LENGTH: 123
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local S
Matches 35
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Best Local S
Matches 16
TITLE OF INVENTION: Expressed Sequence Tage Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patent.pm
SEQ ID NO 16612
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961

FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens -09-513-999C-16612
                                                                                                                        APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
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EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: n =
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L INFORMATION:
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Similarity 67.3%;
35; Conservative
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                                                                                                                                                                                                   Application US/09513999C
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Pred. No. 1.1e
26; Mismatches
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Pred. No. 1.3e+03;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16612
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Best Local Similarity
Matches 35; Conserv
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LENGTH: 181
                                                                                                    Matches
                                                                                                                           Query Match
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                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
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                                                                                                   Local Similarity
nes 38; Conserv
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                                                                                                                                                                                                                                                                                                            NAME: Casuto, Dianne REGISTRATION NUMBER:
                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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91
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Abbott Park
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: NOVEL ANTIANGIOGENIC PEPTIDES,
: POLYNUCLEOTIDES ENCODING SAME
: FOR INHIBITING ANGIOGENESIS
                                                                                                              15.7%;
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67.3%;
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Pred. No. 1.3e
0; Mismatches
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                                                                                                  Score 24.2; DB 3;
Pred. No. 1.8e+03;
); Mismatches 23;
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                                                                                                                           175;
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Sequence 15, Application US/08924287A

Patent No. 6699838

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Davidson, Donald J.

TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME APPLICATION: ANGIOGENESIS

FILE REFERENCE: 5940.US.P3

CURRENT APPLICATION NUMBER: US/08/924,287A

CURRENT FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 08/851,350
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US-08-851-350-15/c
; Sequence 15, Application U
; Patent No. 6057122
; GENERAL INFORMATION:
; APPLICANT: Abbott Labo
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US-08-924-287A-15
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US-08-851-350-15
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Best Local Similarity 62.3%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEPAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,3
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ATTORNEY/AGENT INFORMATION:
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Abbott Park
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: NOVEL ANTIANGIOGENIC PEPTIDES,

: POLYNUCLEOTIDES ENCODING SAME AND METHODS

: FOR INHIBITING ANGIOGENESIS
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Pred. No. 1.8e+03;
D; Mismatches 23;
                                                                                         SAME
                                                                                       AND METHODS
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                                                                                      INHIBITING
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RESULT 17
US-09-513-999C-15749
· Sequence 15749, Application US/09513999C
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                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION:
US-08-924-287A-15
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TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME ANI

TITLE OF INVENTION: ANGIOGENESIS

FILE REFERENCE: 5940.US.P3

CURRENT APPLICATION NUMBER: US/08/924,287A

CURRENT FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: US 08/851,350

PRIOR FILING DATE: 1997-05-05

PRIOR APPLICATION NUMBER: US 08/832,087

PRIOR FILING DATE: 1997-04-03

PRIOR FILING DATE: 1997-04-03
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US-08-924-287A-15/c
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Matches
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PRIOR FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08924287A Patent No. 6699838 GENERAL INFORMATION: APPLICANT: Abbott Laboratories APPLICANT: Davidson, Donald J.
                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-05-05
PRIOR APPLICATION NUMBER: US 08/832,087
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: US 08/643,219
PRIOR FILING DATE: 1996-05-03
NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                  140 G
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                                                                                                                                                                91
                                                                                                                                                                              80 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACGATGAGCGAGAT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 CATCACGGTGGTGGTGTGCCGCGCGCAGCTGAAGAGCTGGCTC
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                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                          Similarity 38; Conserv
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                                                                                                                                                                                                                                      15.7%;
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Pred. No. 1.8e
0; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                       DB 4;
.8e+03;
.es 23;
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.8e+03;
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                                                                                                                                                                                                                                                       175;
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                                                                                                                                                              CACCACCGTGAT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTTCGGGTGGG 90
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; Sequence 15749, Application US/09513999C
; Patent No. 6783961
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                                                                                           ; LOCATION: 45; OTHER INFORMATION: 8=9
US-09-513-999C-15749
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                                                                                                                                                                                                                                                                               SOFTWARE: Patent.pm
SEQ ID NO 15749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
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Best Local Similarity
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SEQ ID NO 15749
LENGTH: 71
                               Matches
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne
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                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                   LENGTH: 71
TYPE: DNA
                                                                                                                                                                        FEATURE:
FEATURE:
NAME/KEY: misc_feature
TON: 35
                                                                                                                       NAME/KEY: misc_feature LOCATION: 45
                                                                                                                                                                      LOCATION: 35
OTHER INFORMATION:
                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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OTHER INFORMATION: r=a
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                                              Local
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                              1 Similarity 62.5
35; Conservative
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CGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCC 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano,
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                                         15.3%;
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                                             Score 23.6;
Pred. No. 2
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Pred. No. 2.4e+03;
L; Mismatches 20;
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                               Mismatches
                             6; DB 4;
2.4e+03;
ches 20;
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                              Indels
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                              Gaps
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Ser
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8568
LENGTH: 195
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US-09-902-540-8568/c
; Sequence 8568, Application US/09902540
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; ORGANISM: Myxococcus
US-09-902-540-8568
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US-09-902-540-8568
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SEQ ID NO 8568
LENGTH: 195
TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                  Matches
                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goldman, APPLICANT: Hinkle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.6
                                                                                                                               Local Similarity
                           137
                                                         162
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o. 6833447
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                           GATGACCAGC 146
                                                      GCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTGACGATGAGCGA 136
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93
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58.6%;
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Pred. No. 2.5e+03;
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Pred. No. 2.5e+03;
); Mismatches 29
                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                       Sequences
                                                                                                                                           Length
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                                                                                                                 Indels
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GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10
RESULT 23
US-08-447-985-14
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US-09-902-540-2996/c
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; ORGANISM: Myxococcus xanthus
US-09-902-540-2996
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US-09-902-540-2996
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Best Local
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LENGTH: 126
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SEQ ID NO 2996
LENGTH: 126
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Best Local Similarity 50.9%;
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Myxococcus
                                                                                                                                                                                                                              Local
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No. 683344
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lo. 6833447
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55; Conservative
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                                                                                                     ATCGTCGAGTCGGCGGCCGCCGACTGACGATGAGCGAGATGACCAGC
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                                                                      ATCAGCGCCGCGGCGAGCAGGATGGAGGCGATGGCCACCGTGACCATC
                                                                                                                                       GCCCACAGCTCGCGCGTGGCCTCATTCTCGCGTTGACGGTTGACGGCGTCTGGATGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGGTCACGGTGGCCATCGCCTCCTGCTCGCCGCGCGCTGATGGGCATCCAGAC
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Pred. No. 3.
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Pred. No. 3.1e+03;
D; Mismatches 53;
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome
                                                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                                             Length 126;
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RESULT 24
US-08-447-985-14/c
; Sequence 14, Application US/08447985
; Patent No. 6399861
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application Patent No. 6399861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION UNMBER: US/08/447,985
FILING DATE: 23-May-1995
CLASSIFICATION **. *Unknown**
PRIOR APPLICATION NUMBER: 08/113,561
APPLICATION NUMBER: 08/113,561
FILING DATE: *Unknown**
APPLICATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION NUMBER: 32,165
REGISTRATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 713/789-2679
TELEFAX: 713/789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                             APPLICANT: Adams, Thomas R. et al. TITLE OF INVENTION: Methods and Compositions for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Adams, Thomas R. et al.
TITLE OF INVENTION: Methods and Compositions for Production of Stably Transfand Cells Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
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6399861
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                 CITY: Houston
STATE: Texas
                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG
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STATE: Texas
COUNTRY: USA
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                                                   P.O. Box 4433
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and Cells Thereof
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Pred. No. 4
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                                                                                                                                              of Stably Transformed
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                                                                                                                                              Fertile Monocot Plants
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RESULT 25
US-08-852-340-14
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GENERAL INFORMATION:
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Best Local (
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                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-MAY-1997
CLASSIFICATION: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
STREET: P.O. Box 443
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                        ALL...
STREET: F...
CITY: Houston
TRATE: Texas
TI.S.
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                                                                                                                                                                                                                       COUNTRY: U.S. ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/113,561
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: DEKM:05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 713/789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,985
FILING DATE: 23-May-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08852340
                                                                                                                                                                                                                                                                                                                                                                   Adams, Thomas R., et al.

/ENTION: METHODS AND COMPOSITIONS FOR THE
/ENTION: PRODUCTION OF STABLY TRANSFORMED,
/ENTION: AND CELLS THEREOF
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                                                                                                                                                                                                                                                                                                              White
                                                                                        US/08/852,340
                  07/113,561
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                                                                                                                            Version
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RESULT 26
US-08-852-340-14/c
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                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DEKM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713)789-2679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (713)789-26/7
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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Best Local &
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-MAY-1997
CLASSIFICATION: 504
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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REFERENCE/DOCKET NUMBER: DEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Texas
COUNTRY: U.S.
ZIP: 77210
                                                             STRANDEDNESS:
TOPOLOGY: li
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TELEPHONE: (512)
TELEPHONE: (713)789-2679
TO NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                                                                           nucleic acid
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llarity 55.8%;
Conservative
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                                                                           single
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HETHODS AND COMPOSITIONS FOR THE
PRODUCTION OF STABLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND CELLS
26
14.7%;
55.8%;
                                                                                                                                                                                                                                                                                 US 07/113,561
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 Score
Pred.
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Pred. No. 4.5e+03;
); Mismatches 34
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22.6; DB 4;
No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
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             Length
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                  185;
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RESULT 28
US-08-622-740-9/c
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US-08-622-740-9
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,740
FILING DATE: 27-MARCH-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.013US4
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-0331
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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            Sequence 9, Application Patent No. 5990390 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5990390
GENERAL INFORMATION:
APPLICANT: Lundqui
APPLICANT: Walters
APPLICANT: Kirihar
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Production of Stably Transformed, TITLE OF INVENTION: and Cells Thereof NUMBER OF SEQUENCES: 22 CORRESPONDERS:
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic ac
STRANDEDNESS: si
TOPOLOGY: linear
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55402
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                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                            AGGGGCTCAAGTCCACCGCCAGCCTCCCCGTCG
                                                                                                                                                          GCGAGATGACCAGCTCCGGCCGGCCGACTCGACG 128
                                                                                                                                                                                                                    GGCGGCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGA
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                                                                                                                                                                                                                                                     14.7%;
larity 52.7%;
Conservative
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Lundquist,
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                                               US/08622740
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Ronald C
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Pred. No. 4.5e+03;
D; Mismatches 44,
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RESULT 29
US-08-440-689-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 49; Conser
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,740
FILING DATE: 27-MARCH-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WOCESSNEY, WATTON
                                                                                                                                                                                                                                                                                                                             Patent No. 6025545
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence
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ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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TITLE OF INVENTION: Me
TITLE OF INVENTION: PI
TITLE OF INVENTION: ar
NUMBER OF SEQUENCES: (
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed,
TITLE OF INVENTION: and Cells Thereof
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                         COUNTRY: USA
ZIP: 55402
                                                                                                             CITY: Minneapolis STATE: MN
                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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5. 6025545
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3500 IDS Center
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larity 52.7%;
Conservative
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Pred. No. 4.5e
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4.5e+03;
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US-08-440-689-9/c
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
TYPE: nucleic single
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Best Local Similarity 52.7%;
Matches 49; Conservative
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                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,689

FILING DATE: 15-MAY-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 950.013US2

TELECOMMUNICATION INFORMATION:
                                     TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
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TELEFAX: 612-339-3061
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5. 6025545
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195 base pairs
ucleic acid
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Kirihara, Julie A.
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                                                                                          612-339-0331
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Pred. No. 4.5e+03;
0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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US-09-122-399-9
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local (
                                                                                                                                                                                                                                             Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
104 AGGGGCTCAAGTCCACCGCCAGCCTCCCCGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 195 base pairs nucleic acid
                                                                                                                                                                            CGTCGAGTCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACCT 86
                                                          GCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
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                                                                                                                      ĠĠĊĠĊĊĊAĊĊĠTĠATĠAĂĊĊĠŦĠAŤĠĂŤĠĠĊĊŦĊĠŤĊĠĠĊĊAĊĊĠĊĊ
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kirihara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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00 IDS Center
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52.7%;
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Production o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ronald C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lundberg & Woessner,
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                                                                                                                                                                                                                                                                          Score 22.6; DB 3; Pred. No. 4.5e+03;
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Pred. No. 4.5e+03;
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Thereof
                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                          DB 3;
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                                                                                                                         GTCGCTCCGTTCC 103
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RESULT 33
US-08-440-646A-9
US-08-440-646A-9
; Sequence 9, Application US/08440646A
; Patent No. 6777589
; GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.:
Walters, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; INFORMATION FOR SEQ ID NO: 9
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-122-399-9
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US-09-122-399-9/c
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Best Local S
Matches 49
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GENERAL INFORMATION:
APPLICANT: Lundqui
APPLICANT: Walters
APPLICANT: Kirihar
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FILING DATE:

CLASSTETT: CLASSTETT: CLASSTETT: CLASSTETT: CIPROPY disk

COMPUTER: IBM PC compatible

CCASTON PC compa
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
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Local Similarity 52.7%;
les 49; Conservative
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  NUMBER OF
                                                                                      TITLE
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                INVENTION: Methods and Compositions
Production of Stably Trar
and Cells Thereof
SEQUENCES:
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00 IDS Center
                                                                                                             Walters, D
Kirihara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESS:
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-1993
                                                                                                                                              t, Ronald C.
David A.
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Pred. No. 4.5e
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                                                Fertile Monocot
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US-08-440-646A-9/c
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                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08440646A Patent No. 6777589
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION DATA:
APPLICATION UMBER: US/08/440,646A
FILING DATE: 15-May-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION UMBER: 30,440
REGISTRATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                      NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
                                                                                                                                                                                                                                                                                         APPLICANT: Lundquist, Ronald C.
Walters, David A.
                                                                                                                                                                                                                                                           TITLE
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ADDRESSEE: Schwegman, Lundberg
STREET: 3500 IDS Center
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                                                                                                                                     CITY: Minneapolis
                                                                                                                                                                                                           Kirihara, Julie A.

OF INVENTION: Methods and Compositions for the Production of Stably Transformed, and Cells Thereof
                                                                                                           COUNTRY: USA
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Center
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0; Mismatches
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      Version
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RESULT 35
US-08-105-168B-6
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COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: August 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION UMBER: FR9210094
FILING DATE: August 8, 1992
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEPHONE: (703) 836-2787
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH. 200 base 2502
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APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-0331
TELEFAX: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
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Best Local S
Matches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA,
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES,
TITLE OF INVENTION: MYCOBACTERIA
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexandria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Oliff & Berridge 700 South Washington Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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52.7%;
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Pred. No. 4.5e+03;
); Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite 300
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REAGENTS AND METHOD FOR THE DET
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US-08-105-168B-6/c
; Sequence 6, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
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                                                                                              COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
FILING DATE: August 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: FR9210094
FILING DATE: August 8, 1992
APPLICATION NUMBER: 992
APPLICATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WBB 28835
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                  TELEPHONE: (703) 836-640
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: Oliff & I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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HYPOTHETICAL:
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ZIP: 22314
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium intralcellulare
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Similarity 57.1%;
60; Conservative
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                                  200 base pairs
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JENTION: DNA FRAGMENTS OF MYCOBACTERIA,
JENTION: PRIMERS, HYBRIDIZATION PROBES,
JENTION: MYCOBACTERIA
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single-stranded
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Pred. No. 4.5e+03;
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REAGENTS AND METHOD FOR THE DETI
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US-08-698-948-6
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Best Local Similarity
TELEFAX: (703) 836-2787 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                          APPLICATION NUMBER: 08/105,168
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: POSITION IN GENOME: CHROMOSOME/SEGMENT:
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ORGANISM: Mycobacterium
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: August 16
                                             REFERENCE/DOCKET NUMBER: WPB 28835A TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                         CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                REGISTRATION NUMBER:
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August 16, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA FRAGMENTS OF MYCOBACTERIA, PRIMERS, HYBRIDIZATION PROBES, MYCOBACTERIA
                                                                                                                                                                                                                                                                                                                          MS DOS 3.1
                                                                                           30,024
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 200;
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REAGENTS AND METHOD FOR
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Best Local Similarity 57.1%;
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168
PILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MABILAT et al.
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA,
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES,
TITLE OF INVENTION: MYCOBACTERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Myc
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TOPOLOGY: lir
MOLECULE TYPE:
                                              NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible OPERATING SYSTEM: MS DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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                              ELECURAL: (703)
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IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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    CHARACTERISTICS:
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N: 536
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16, 1996
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Pred. No. 4.5e+03
); Mismatches 4
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genom
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8045
LENGTH: 174
TYPE: DNA
RESULT 40
US-09-902-540-8045/c
; Sequence 8045, Application US/09902540
; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-09-902-540-8045
; Sequence 8045, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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; LOCATION: 518-717
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-698-948-6
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Best Local Similarity 59.4%;
Matches 38; Conservative
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Best Local (
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HYPOTHETICAL:
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Similarity 57.1%;
50; Conservative
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Pred. No. 5e+03;
D; Mismatches 26;
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Pred. No. 4.5e+03;
0; Mismatches 44
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APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sec.

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 8045

LENGTH: 174
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Seq.

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7303
US-09-902-540-7303/c
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                   RESULT 42
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Best.Local S
Matches 40
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Patent No.
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Best Local S
Matches 38
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LENGTH: 102
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Pred. No. 6.1e+03;
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Pred. No. 5e+03;
); Mismatches 26;
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; Sequence 7303, Application U
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S
; APPLICANT: Hinkle, Gregory
; APPLICANT: Slater, Steven

US/09902540

Barry S. Gregory J. Steven C.

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APPLICANT: Ito, Laura Y.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY

FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SOFTWARE: PERL Program

SEQ ID NO 6924
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                                                                               RESULT 44
US-09-313-294A-6924/c
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7303
LENGTH: 102
                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 52
Sequence 6924, Application Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghu APPLICANT: Ito, Laura Y.
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Best Local :
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700380851H1
NAME/KEY: unsure
LOCATION: 22, 60, 64, 76, 83, 85
OTHER INFORMATION: a, t, c, g, or other
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TYPE: DNA
ORGANISM: Zea mays
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RESULT 45
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APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome See

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
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CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6924
LENGTH: 164
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GENERAL INFORMATION:
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least on target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous
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                            New recombinant construct having a promoter operably live sequence which when expressed produces an RNA having how mRNA and its reverse complement unrelated to endogenous
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RESULT 4
AAD32908/c
ID AAD32908 standard; DNA; 154 BF
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AC AAD32908;
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DT 01-JUL-2002 (first entry)
XX
DE Plasmid pKS133 2X BLVISLIVES C
XX
KW Rice; diverged delta-9 fatty a
KW oil; transgenic plant; gene ma
KW os Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The present invention relates to diverged delta-9 fatty acid desaturase CC proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular CC lipids, including oil, in tissues when the enzyme is absent or rate-CC limiting, to isolate cDNAs and genes encoding homologous proteins from CC the same or other plant species and to create transgenic plants in which CC the polypeptides are present at higher or lower levels than normal or in CC cell types or developmental stages in which they are not normally found, CC thus altering the level of mono-, poly- and unsaturated fatty acids in CC those cells. They are useful as probes for genetic and physical gene CC (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133 CC This sequence is used in the exemplification of the invention for the Suppression of Fad2 in sowhear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
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                                                                                                                                                                                                     Plasmid pKS133 2X ELVISLIVES complementary repeat
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Pred. No. 2.7e-28;
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                                                                                                                                                                    Query Match
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                     ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG
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llarity 100.0%;
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RESULT 5
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construct operated the plant, an isoflavonoid-containing product, and a method of
construct operated the isoflavonoid-containing product, and a method of
constructing an isoflavonoid-containing product having a reduced ratio of
construct acid sequence forms a loop in the stem-loop structure. The
construct acid sequence of ADQ07968). The promoter is a seed-specific
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The invention relates to decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavonoid-producing plant comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid sequence of at least 200 nucleotides having at least 75% sequence identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included are an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has incorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product, and a method of liquiritigenin-derived isoflavone relative to the total isoflavone levels. The recombinant construct comprises a stem-loop structure and the nucleic acid sequence forms a loop in the stem-loop structure and the stem comprises a sequence of aDQ07968). The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin calculative to the total isoflavones in an isoflavone-conducing plant. The methods and recombinant construct are useful in producing an isoflavonoid-containing product.
                  RESULT 6
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ADQ07968/
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ADQ07968
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Example

19;

27pp;

English

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ABK10711/c
ID ABK10711;
XX
AC ABK10711;
AC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       their related nucleic acids. The sequences are useful for producing a CC transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. CC phosphoglucomutase activity. An isolated polynucleotide that affects the cc phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a cc plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide with the level of the polypeptide in the polypeptide in a plant cell that does not contain the collated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comparises consisted polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered comparisor of plastidic phosphoglucomutase. This sequence represents an convention of altered convention.
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Best Local S
Matches 81
                                                                                                                      17-JUL-2001;
                                                                           17-JUL-2000; 2000US-0218712P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plastidic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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'product= "ELVISLIVES peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "ELVISLIVES
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                              NEMOURS
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100.0%; Pr
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant; gene;
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RESULT 9
AAD29230
ID AAD2
XX
AC AAD2
XX
DT 07-M
XX
DE Plas
XX
CW Recc
KW CDS
FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a common transferming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of compression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in the polypeptide in the plant cell containing the isolated polynucleotide with the isolated polynucleotide. The isolated polynucleotide with the level of the polypeptide in a plant cell that does not contain the isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered convention of plastidic phosphoglucomutase. This sequence represents an convention in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                    Unidentified
                                                                                                                                                                                                                           Plasmids pKS106,
                                                                                                                                                                                                                                                                                       AAD29230;
                                                                                                                                                                                               Recombinant
                                                                                                                                                                                                                                                          07-MAY-2002
                                                                                                                                                                                                                                                                                                                    AAD29230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptides having phosphoglucomutase polynucleotides encoding the polypeptides, useful for transgenic plants with altered plastidic phosphoglucon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                CGAGATGACCAGCTCCGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Butler KH,
                                                                                                                                                                                               construct;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
llarity 100.0%;
Conservative (
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                             complement(45..74)
/*tag= b
/product= "ELVISLIVES p
                                                                                                        Location/Qualifiers
7. .36
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                                                                                                                                                                                                                                                                                                                     DNA;
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                             "ELVISLIVES protein"
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; Pred. No. 1.3
0; Mismatches
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                                                                                                                                                                                              plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                               pKS124;
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                                                                                                                                                                                              plasmid pKS106;
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WO200200904-A2

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RESULT 10
AAD29230/c
ID AAD29230;
XX
AC AAD29230;
XX
OT-MAY-200
XX
DE Plasmids 1
XX
KW Recombinan
KW ds.
XX
OS Unidentif:
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FH Key
FT CDS
FT CDS
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Best Local
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least on target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 1% ELVISLIVES complementary repeat region D found in plasmids pKS106 and pKS124 used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glassman
Nichols S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant construct having a promoter operably linked to a sequence which when expressed produces an RNA having homology to mRNA and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-139927/18.
P-PSDB; AAE18333.
                                                                                                          Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                       07-MAY-2002
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                                                                       Unidentified
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PIONEER
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SE;
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Similarity 100.0%;
80; Conservative (
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                                                                                                                               pKS106,
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/product= "ELVISLIVES
complement(45. .74)
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                                              Location/Qualifiers
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                                                                                                        expression; plasmid pKS124;
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            protein"
                                                                                                                               complementary repeat
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,. 2.2e-10;
0;
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a target
reducing
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RESULT 11
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the sequences and their reverse genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106 and pKS124 used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant construct having a promoter operably sequence which when expressed produces an RNA having mRNA and its reverse complement unrelated to endogency gene expression.
                                                                                                                                                                                                                                                                                                                                              Sequence
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P-PSDB; AAE18333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PION-)
                               Diverged delta-9 fatty acid desaturase; transgenic plant; gene mapping; immunisa plasmid pKS106; gene; ds.
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                                                                                                                                                  AAD32907
          Unidentified
                                                                              Plasmids pKS106, pKS124 1X
                                                                                                     01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
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PIONEER
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SE;
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                                                                                                                                                                                                                              GAGATGACCAGCTCCGGCCG 117
                                                                                                                                                                                                                                                                            CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGA
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                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                  standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                BP;
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HI-BRED INT INC.
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/product= "ELVISLIVES protein"
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Pred. No.
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                                             immunisation; p
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2.2e-10;
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                                             plasmid
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                                             lipid; oil;
S124;
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                                                                              at DNA.
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RESULT 12
AAD32907/c
ID AAD32907;
XX
AC AAD32907;
XX
DT 01-JUL-200
XX
DE Plasmids 1
XX
KW Diverged 0
                                                                                                                                                                                                                                                                                                                                     proteins and polynucleotides encoding such proteins. The nucleic acid controls are proteins and polynucleotides encoding such proteins. The nucleic acid controls are may be used to increase the level of unsaturation in cellular controls, including oil, in tissues when the enzyme is absent or rate.

CC limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene capping and as markers, e.g. restriction fragment length polymorphism companies specific for the peptides can be used to immunise animals to produce is 1x ELVISLIVES complementary repeat region DNA found in plasmids pXS106 and pXS124. This sequence is used in the exemplification of the invention controls of the invention of the suppression of Fad2 in soybean
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Matches 80
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P-PSDB;
                                                                                                                                                                                                                                                                                                                       Sequence
                                                   01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, pol - and unsaturated fatty acids and in increasing the unsaturation levels in cellular lipids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
CDS
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                                                                                                                                                                     13
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                                                                                                                                                                                                                                                                       80;
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                                                                                                                                                                                                                                                                                  Similarity
                          pKS106,
                                                                                                                                                                                                                                    CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
  delta-9
                                                                                                    standard; DNA;
                                                                                                                                                                    GAGATGACCAGCTCCGGCCG
                                                                                                                                                                                   GAGATGACCAGCTCCGGCCG-117
                                                                                                                                                                                                                                                                                                                        08
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                          pKS124 1X
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                        ELVISLIVES complementary repeat DNA
                                                                                                     ВP
 desaturase;
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. 2.2e-10;
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  enzyme;
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cellular
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oil;
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RESULT 13
ABK10712
ID ABK10
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AC ABK10
XX

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ВP

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ABK10712; ABK10712

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Matches 80
                                                                                                                                                                              The present invention relates to diverged delta-9 fatty acid c proteins and polynucleotides encoding such proteins. The nucleotides may be used to increase the level of unsaturation continuiting, including oil, in tissues when the enzyme is absented in intiting, to isolate cDNAs and genes encoding homologous protect the same or other plant species and to create transgenic plant could the polypeptides are present at higher or lower levels than increase the polypeptides are present at higher or lower levels than it is polyes or developmental stages in which they are not now thus altering the level of mono-, poly- and unsaturated fatt; those cells. They are useful as probes for genetic and physic mapping and as markers, e.g. restriction fragment length polic (RFLP) markers. The peptides can be used to immunise animals antibodies specific for the peptides and proteins. The present is 1x ELVISLIVES complementary repeat region DNA found in place and pks124. This sequence is used in the exemplification of for the suppression of Fad2 in soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                      New delta-9 fatty acid desaturase polypeptides and polynuseful in creating transgenic plants having altered level - and unsaturated fatty acids and in increasing the unsatin cellular lipids.
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P-PSDB; AAE20554.
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20
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                         GAGATGACCAGCTCCGGCCG
                                                   CGGCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGCCGAC
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                                                                                                    51.9%;
llarity 100.0%;
Conservative
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/product=
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                                                                                                    Score 80; DB; Pred. No. 2.2 0; Mismatches
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levels of mono-, poly
unsaturation levels
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proteins from
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                                                   TCGACGATGAGC
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                                                                                                    Gaps
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RESULT 14
ABK10712/c
ID ABK10712:
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AC ABK10712:
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AC ABK10712:
XX
OT 05-JUN-20
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                                                                                                                                                                                                                                                                                                        The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a contranspenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of compression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the level of the polypeptide in a plant cell containing the level of the level of the polypeptide in a plant cell that does not contain the collated polynucleotide. An a plant cell that does not contain the lastidic phosphoglucomutase protein in a host cell comprises cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered collavels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction, in the methods of the
                                                                                                                                  문
                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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    05-JUN-2002
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                                                                                                                                                                                                            CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC
                                                                                                                                                                                                                                                                                                        92
                                                           standard;
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                                                                                                                                                                                                                                                                                                       вP;
                                                                                                                                                                                                                                             51.9%; S. larity 100.0%; Conservative 0;
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   (first entry)
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                                                                                                                                                                                                                                                                                                       Other;
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RESULT 15
AAD29232
ID AAD29
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AC AAD29
XX
AC AAD29
XX
XX
O7-MA
XX
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AAD29232 st. AAD29232; 07-MAY-2002

(first

entry)

standard;

DNA;

92

ВP

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                                                                                                                 Best Loc
Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic
levels.
                                                                                                                                                                        Sequence
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                                                                                                                              Similarity
                    GAGATGACCAGCTCCGGCCG
                                                                                   CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGA
                                                                                                                                                                         92
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                                                                                                                                                                        BP;
                                                                                                                 Conservative
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                                                                                                              Score 80; DB Pred. No. 2.2 0; Mismatches
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2.2e-10;
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                                                                        CTCGACGATGAGC
                                                         CTCGACGATGAGC 27
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RESULT 16
AAD29232/c
ID AAD29
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AC AAD29
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DT 07-MA
XX
DE ELVIS
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DE ELVIS
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CM Recom
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Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glassman
Nichols S
 WO200200904-A2
                                             Recombinant
                                                                     ELVISLIVES
                                                                                             07-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant construct having a promoter operably linked to sequence which when expressed produces an RNA having homology terminal and its reverse complement unrelated to endogenous DNA, for
                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression.
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SE;
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                                                                                                                                                                                                                                                                                                                                             92
                                                                   complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 37;
                                             construct;
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                                                                                                                                                                                                                                                                                                Conservative
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                                             expression;
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hes 0;
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                                            primer;
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RESULT 17
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AC ABK10
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DT 05-JU
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DE Artif
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Plast
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FT CDS
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  EP1174510-A2
                                                                                             Synthetic.
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Nichols S
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RNA and its reverse
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PIONEER
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llarity 100.0%;
Conservative
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                                                                       Location/Qualifiers
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HI-BRED INT
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                    stop codon
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                                        peptide"
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. 2.2e-10;
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                                                                                                                 plant;
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ology to a target
DNA, for reducing
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RESULT 18
ABK10710/c
ID ABK10710 6
ABK10710
ID ABJ
XX ABJ
XX OS
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XX Pla
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic posphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the polypeptide in the plant cell containing the level of the polypeptide with the level of the polypeptide in a plant cell that does not contain the collated polynucleotide. A method for altering the level of expression of the plastidic phosphoglucomutase protein in a host cell comprises can plastidic phosphoglucomutase protein in a host cell comprises transformed cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered levels of plastidic phosphoglucomutase. This sequence represents an convention in the methods of the
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase proteing
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                                                                              Synthetic
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                                                                                                        Plastidic
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                                                                                                       phosphoglucomutase;
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llarity 100.0%;
Conservative (
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                                                   Location/Qualifiers
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Human

brain

Н

calcium

channel alpha

1G

subunit

0

channel; human;

subunit;

epilepsy;

drug

screening;

brain

н

calcium channel;

alpha

5

subunit; 16.

WO200070044-A2

sapiens

07-MAR-2001

(first

entry)

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RESULT 19
AAC89216
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to plastidic phosphoglucomutase polypeptides and CC their related nucleic acids. The sequences are useful for producing a CC transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of CC Polynucleotide fragments are useful for suppressing the level of CC expression of a gene encoding a polypeptide having plastidic phosphoglucomutase polypeptide in a CC level of expression of a plastidic phosphoglucomutase polypeptide in a CC least 541 nucleotides, measuring the level of the polypeptide in the CC plant cell containing the polynucleotide, and comparing the level of the level of the polypeptide in a plant cell that does not contain the CC polypeptide in the plant cell containing the level of the level of the polypeptide in a plant cell that does not contain the CC isolated polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises CC a plastidic phosphoglucomutase protein in a host cell comprises CC cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered CC levels of plastidic phosphoglucomutase. This sequence represents an CC invention
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                                        AAC89216
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
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Best Local S
Matches 51
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AAC89216
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                                    13-MAY-1999;
04-JUN-1999;
                                                                                                                                                                    Human
                  ( OLYU)
                                                                                                    WO200070044-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Splice variants of the human brain II subunits and genes encoding the antiepileptic drugs or for testing
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04-JUN-1999;
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                                                                                                                                                channel; human;
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DB; AAB50116.
                                                                                                                                                                    brain
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99US-0137547P.
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                  HOPKINS
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drug screening;
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Pred. No. 4.2e
0; Mismatches
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4.2e+02;
ches 36;
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Best Local S
Matches 51
Novel purified corn-ear derived polynucleotide useful probe for detecting polynucleotide in sample, and for evaluating, and altering desired characteristics associativelopment.
                                                                                                                                                                                                                                                             Corn ear-derived polynucleotide; structural gene; functional gene corn ear-specific profile; gene thybrid plant; desirable trait expended inheritance; desired characteristic disease resistance; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sechuman brain T calcium channel alpha 1G and alpha 1I subur 1G subunit gene (designated CACNAIG) consists of 38 exons alternative processing leads to the production of 64 diff The alpha 1I subunit (designated CACNAII) consists of 37 proteins are produced due to alternative processing. The provided by the invention are useful for screening drugs
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                                                                                                                                                                                                                                                                                                                                              ear-derived polynucleotide (cpd)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of epilepsy
                                                                                                                                                                                                                                                           ene; functional gene; regulatory gene; cific profile; gene transcription; gene expre; desirable trait expression; plant breeding desired characteristic; growth; development; stance; environmental adaptability; quality;
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                                                                                                           GENOMICS
                                                                                                                                                        99US-00313294
                                                                                   ΙY,
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Pred.
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fferent proteins.
7 exons, and 8
e sequences
s for use in the
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                                                                                                                                                                                                                                                                                                 ession;
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growth

hybridization

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RESULT 22
ABX88193/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022

Cc and SATMON023. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are cc useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in cc inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding cc programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth cand development, disease resistance, environmental adaptability, quality, cand yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cdps are also useful in diagnostic assays to compare the corn and techniques. They are also useful in diagnostic assays to corn confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived cornected of cornat directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 64
                                                                                                                                                             Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SA structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding program; inheritance; desired characteristic; growth; development; disease resistance; environmental adaptability; quality; yield;
                                                                                                                                                                                                                                                                                                                      24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                         ABX88193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/psipsDIDEntry.html
                 14-MAY-1999;
                                                05-NOV-2002.
                                                                                                                                                  multigene
                                                                                                                                                                                                                                                                                      Corn
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                                                                                 US6476212-B1
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                                                                                                                                                                                                                                                                                  ear-derived polynucleotide (cpd) #6653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCAGGAGCAAGATGGGTGCCGGCGGCAGGATGACCGAGAAGCAGCGGGAGAAGCAGGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACGATGAGCGAGATGACCAGCTCCGGCCGACTCGACGATGAGCGAGATGACCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTC
                                                                                                                                                trait; plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                     (first entry)
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                 9908-00313294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
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cDNA libraries SAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 197;
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RESULT 23
AAL44709
ID AAL4
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AC AAL4
XX
DT 03-M
XX
DT Huma
XX
DE Huma
XX
TW Huma
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022 cand SATMON023. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in cinbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desirable traits through plant breeding studying inheritance of desirade characteristics associated with growth and yield of corn. The cdps are also useful as molecular markers for the cpds are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to of cdp expression. ABX81541-ABX81440 represent corn ear-derived polynucleotides (cpds) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
               Human; glutamate receptor delta-1 subunit; epilepsy; brain damage; neurodegenerative disorder; Huntington's disease; Parkinson's disease; Alzheimer's disease; schizophrenia; mood disorder; dementia;
                                                                                                                                                                                 AAL44709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with growth,
                                                                                Human
                                                                                                                03-MAY-2002
                                                                                                                                                  AAL44709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/psipsDIDEntry.html
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                                                                               glutamate
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                                                                                                                                                                                                                                                                                                                                standard; DNA;
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                                                                                receptor delta-1
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                                                                                                                entry)
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Pred. No.
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                                                                                sequence
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                                                                                                                                                                                                                                                                                                                                  TCGGGCGGACACC 68
                                                                                                                                                                                                                                                                                                                                                                                                  CCCATCTTGCTCC 128
                                                                                  SEQ ID NO:
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RESULT 24
AAL44709/c
ID AAL447
AC AA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                             Human; glutamate receptor delta-1 subunit; epilepsy; brain damage; neurodegenerative disorder; Huntington's disease; Parkinson's disease Alzheimer's disease; schizophrenia; mood disorder; dementia; neuropathological pain; pain; receptor; anticonvulsant; nootropic; neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL44709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a human glutamate receptor delta-1 subunit polypeptide. This can be used to screen for agents which modulate the activity of glutamate receptor delta-1 subunit polypeptide, which may then be used in the treatment of diseases such as epilepsy, brain damage, neurodegenerative disorders such as Alzheimer's disease, Huntington's disease and Parkinson's disease, schizophrenia, mood disorders, pain, neuropathologic pain and dementias. The present sequence is a fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human glutamate receptor delta-1 subunit protein which can regulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, benign prostate hyperplasia and urinary
                                                                           WO200206313-A2
                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2002.
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uropathic; antiparkinsonian;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTCAACGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 41
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                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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Pred.
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vulnerary; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 G;
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No. 26
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plasia and urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
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RESULT 25
AAL44706
ID AAL44
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AC AAL44
AC AAL44
DT 03-MI
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DE Huma
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Huma
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Huma
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RW neur
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XW 24-
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PD 24-
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PF 13-
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PPR 18
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                                                                                                                                                                                                                                                                                                                                                             Human
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                                     Kossida
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                                                      Novel human glutamate receptor delta-l subunit protein which can legulated for treating epilepsy, schizophrenia, neurodegenerative diseases, ischemia, pain, beniqn prostate humaniania
                                                                                                                                                                                                                                                                                          Alzheimer's disease; schizophrenia; mood disorder; dementia; neuropathological pain; pain; receptor; anticonvulsant; nootropic; neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic; uropathic; antiparkinsonian; vulnerary; gene; ds.
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ilarity 60.3%;
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                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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sy, brain damage,
Huntington's
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RESULT 28
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DT 06-OCT-200
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CC The preser obtaining pr diagnostic
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CC Sequences
CC They are cc cc copy are copy
                           S
                                                                                                                                                           identified within the present sequence. The 5' ESTs were prepared from CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA CC libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used in obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in CC diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic,
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195
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                            The invention relates to human breast cancer expressed polynucl (AAL07544-AAL26789) and methods of assessing whether a patient afflicted with breast cancer by examining the correlation betwe expression of certain markers and the cancerous state of breast The polynucleotides and encoded polypeptides are potential mark detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and e polypeptides are also useful for isolating compounds with cytos
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09-JUN-2000;
25-JUL-2000;
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
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2.8e+03;
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RESULT 30 AAL17387/c ID AAL17387

standard;

CDNA;

170

ВP

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RESULT 31
AAL09498
ID AAL0
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DT 07-I
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
25-JUL-2000;
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activity
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50; Conservative
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                     marker;
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Pred. No. 2.8e+03;
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                    cytostatic;
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RESULT 32
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Matches 50
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14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                               Human
                                                                                                                                                                                      AAL09498
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                                     10-JAN-2001;
                                                       19-JUL-2001.
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activity
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50; Conservative
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                                                                                                                                                                                      standard;
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                                                                                                              cytostatic;
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|CGTCCGGCCGCA 92
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RESULT 33
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ID AAT49
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15-MAY-2000;
09-JUN-2000;
25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          Filamentous; fungus; Byssochlamys nivea; Neosartorya fischeri; pr. Zygosaccharomyces bailii; PCR; amplification; polymerase chain reprises internal transcribed spacer; detection; heat resistant; microorganism; contaminant; strawberry; foodstuff; ss.
                                                                                                                                                                                                                                         31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                     Neosartorya fischeri
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nilarity 55.6%;
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2.8e+03;
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contaminants

derived

from

n internal transcribed spacer ser of foodstuffs, esp Byssochlamys

sequences

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 Neosartorya used

ganisms of especially

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RESULT 34
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AC AAT49353;
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Best Loc
Matches
          The invention relates to methods to detect the filamentous fungi Byssochlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii by PCR amplification on genomic DNA using primers derived from the ribosomal internal transcribed spacer (ITS) sequences (see AAT49351-6). This sequence represents the ITS1 from N. neosartorya and is amplified by the primers AAT49359-60. The method is used to detect heat resistant microorganisms of the above species which are important contaminants of
                                                                                                                                                                                                                                     WPI; 1997-034393/03
                                                                                                                                                                                                                                                                                                                                                              31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neosartorya fischeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filamentous; fungus; Byssochlamys nivea; Neosartorya fisc
Zygosaccharomyces bailii; PCR; amplification; polymerase
ribosomal internal transcribed spacer; detection; heat re
microorganism; contaminant; strawberry; foodstuff; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N. fischeri
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                                                                                                                                                                     s derived from internal transcribed spacer secontaminants of foodstuffs, esp Byssochlamys ri or Zygosaccharomyces bailii.
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                                                                                                                                          18pp; French.
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haromyces bailii by
d from the ribosomal
9351-6). This
is amplified by the
t resistant
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chain reaction;
esistant; fruit;
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    used to
    Neosartorya

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RESULT 35
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                    cown mRNA. The fusions are made by synthesis and in vitro or in situ translation of an mRNA molecule with a peptide acceptor attached to its 3, end. The RNA-protein fusions are incubated under high salt conditions to produce a protein library. This method is useful for improving or altering existing proteins, as well as for isolating new proteins and nucleic acid or small molecule targets. It may also be used to improve human or humanised single-chain antibodies for the treatment of a number of diseases. The method is useful for the isolation of proteins with specific binding properties, for screening cDNA libraries and cloning new method does not rely on maintaining the integrity of an mRNA: ribosome: nascent chain ternary complex, which is very fragile and is therefore of limited use. The method does not rely on topological links between the protein and the nucleic acid so that the information of the protein is retained and can be recovered in readable, nucleic acid form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 43
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                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                      existing proteins, by in vitro translating produce RNA-protein fusions and incubating high salt conditions.
                                                                                                                                                                                                                                                                                                                Producing protein or DNA libraries which are useful for improving existing proteins, by in vitro translating protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1999;
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Sequence
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                                                                                                                                                                                                                                                             Page 72; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion;
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15 C;
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No. 3.5e+03;
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these protein fusions under
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81 Other;
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Query Match Best Local Similarity

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                                                  altering existing proteins, as well as for isolating new proteins and nucleic acid or small molecule targets. It may also be used to improve human or humanised single-chain antibodies for the treatment of a number of diseases. The method is useful for the isolation of proteins with specific binding properties, for screening cDNA libraries and cloning new genes on the basis of protein-protein interactions. Unlike prior art, the new method does not rely on maintaining the integrity of an mRNA:ribosome:nascent chain ternary complex, which is very fragile and is therefore of limited use. The method does not rely on topological links
                                                                                                                                                                     tusions, which comprise a protein covalently linked to the own mRNA. The fusions are made by synthesis and in vitro translation of an mRNA molecule with a peptide acceptor a 3' end. The RNA-protein fusions are incubated under high to produce a protein library. This method is useful for including aviation are incubated.
                                                                                                                                                                                                                                                                                                     existing process, -- nroduce RNA-protein fusions
                            therefore of limited use. The between the protein and the protein is retained and can
                                                                                                                                                                                                                                The present sequence was used in a method fusions, which comprise a protein covalent
                                                                                                                                                                                                                                                                        Disclosure;
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   Sequence
                                                                                                                                                                                                                                                                                                                           Producing protein or DNA libraries which existing proteins, by in vitro translating
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                                                                                                                                                                                                                                                                                                   high salt conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCGCTCATCGTCGAGTCGGCGGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOSPITAL
                                                                                                                                                                                                                                                                        Page 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PP.01.
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                          that the infi
readable, nu
     81
                                                                                                                                                                                                                                generating linked to the
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    Other;
                             topological links information of the nucleic acid form
                                                                                                                                                                                        or in situ
attached to its
salt conditions
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                                                                                                                                                                             improving or
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                                                                                                                                                                                                                                RNA-protein e 3' end of its
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RESULT 37
ACH88658
ID ACH88
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ACH88
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contributes and the problem of the place of a stringer expressed in human cells or tissues. Also included are a spatially-
conditions to a nucleic acid molecule
contributes and the stringer conditions to a nucleic acid molecule
contributes and the stringer conditions to a nucleic acid molecule
contributes and the single exon nucleic acid probes for measuring human
contributes cited above, where each of the plurality of probes is separately
contributes and addressably isolatable or amplifiable from the plurality), a single
contributes an order expression, a vector comprising the single exon
contiguous amino acids of any of the above-mentioned amino acid
contiguous amino acids of any of the above-mentioned amino acid
contiguous amino acids of any of the above-mentioned amino acid
contained antibody that binds specifically to a peptide cited above,
contained antibody that binds specifically to a peptide cited above,
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contained antibody that binds specifically to a peptide cited above,
methods of selling and/or licensing single exon probes or microarrays to
contained the prosession data by subscription, and a computer-readable
contained the probe, methods and apparatus are useful in gene
contend above. The probes may be used as tools for surveying
contissues to detect the presence of expression of a single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human genome-derived single exon nucleic acid probes useful for hum-
gene expression analysis, for identifying or characterizing alternative
splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid probe for measuring human expression, comprising any of the 27,400 fully defined nucleotide
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(RANK/)
(HANZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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RANK D R.
HANZEL D K.
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c alteration.
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RESULT 38
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      rhe invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that comparising a plurality of a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-cadressable set of single exon nucleic acid probes for measuring human cells or gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid substantials.
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sequences
isolated a
                                                                                                                                                                                                                                                                                      New human genome-derived single exon nucleic acid probes
gene expression analysis, for identifying or characterizi
splicing events, for assessing genomic alterations or as
                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 21853; 80pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                smaller genomic alterations, in priming the synthesis cor in expressing the ORF-encoded peptide. The present single exon probe of the invention. Note: The sequence patent did not form part of the printed specification, in electronic format directly from USPTO at sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-119264/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2002; 2002US-00029386
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                                                                                                                                                                                                                                                                              tissues.
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                            s or fragments, and amino acid sequences single exon probe that cleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of nucleic acids,
sequence is a human
e data for this
, but was obtained
                                                                                                                                                                                                                                                                                        useful for human ing alternative tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108;
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above.

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RESULT 39
ACD96616
ID ACD96
XX
ACD96616
XX
ACD96616
AC ACD96
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ACD96
AC ACD96
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ACD96
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing the human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene cxpression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising calterations in the genomic locus that includes their exon, in assessing salterations in the genomic locus that includes their exon, in assessing calterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human calculated that did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Open reading frame detection; genome sequencing; colon cancer; breast cancer; population genome analysis; genetic shift; cancer; antibiotic resistance; antibiotic non-tolerance; congenital disease; agriculture; food crop genome; resistance gene; retrovirus;
                                                                                                                    Determining open reading frames of genome of an organism e.g. suffering from cancer involves use of single oligonucleotide plow stringency for preparing single-stranded cDNA from mRNA of individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002155438-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACD96616
                                                                                                                                                                                                                                                                      WPI; 2003-182626/18
                                                                                                                                                                                                                                                                                                                                                                                                                    (SIMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer cell expressed cDNA #5028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                             SIMPSON A J
                                                                                                                                                                                                                                                                                                                                                                                         BRENTANI R R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCTGGTCTCCCGGCTCCGAGGCGAGGCGCGGCAGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.1%;
ilarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                           Neto ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00196716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00406117.
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                                                                                                                                                                                                                                                                                                                             Brentani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24.8; D
Pred. No. 5.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3e+03;
nes 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypanosome; Plasmodium;
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nucleic sequence of an open reading frame; for preparing a contig,
conucleic acid molecule from a genome of an organism; and for sequencing
control all or part of a genome of an organism. mRNA is obtained from mammalian
cor human cell which is associated with a pathological condition e.g. a
colon cancer or breast cancer cell. The method is useful for analyses of
copulations of subjects and can be used to carry out genetic analyses of
copulations of subjects and can be used to study living
systems to determine if, e.g. there have been genetic shifts which render
condiseases such as cancer, to determine antibiotic resistance or non-
conference, and so forth. The method can also be used in the study of
through ova or sperm. The analyses for pathological conditions can be
conferenced out in all animals, plants, birds, fish, etc. Using this method,
conference can also be studied in this way. Similarly, the method permits
condition of the pathogens which integrate into the genome, such as
conditions or mutations, which may require different approaches to
therefore shifts or mutations, which may require different approaches to
therefore shifts or mutations, which may require bathogens, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single-stranued control and repeating the control resulting and sequencing the product, and repeating the control resulting and amplifying steps with different primers and sequencing resulting and amplifying steps with different primers and sequence from a useful for: determining that a known nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a control of the control of the product of the control of the product of the control of the product of the control of the control of the product of the control of the control of the product of the control of the cont
Sequence
                                                                                  therapy. This method is also applied to eukaryotic pathogens, such as trypanosomes, different types of Plasmodium, etc. The method essentially eliminates sequencing of non-coding portions. This sequence represents a polynucleotide isolated from human colon cancer cell cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the genome of organism, comprising contacting mRNA with a single oligonucleotide primer (I) at low straingle-stranded cDNA by reverse transcribing mRNA v
   130
   B₽;
   28
A; 44 C;
   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer (I) at low stringency, preparing transcribing mRNA with (I), amplifying and repeating the contacting, preparing
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23
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U; O
   Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell of organism
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a known
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Query Match Best Local : Matches 44; Similarity 16.1%; ilarity 57.9%; Conservative 0; Score 24.8; Pred. No. 5. ed. No. 5.4e+03; Mismatches 32; DB 10; Length Indels 130; <u>,</u> Gaps

밁 S 밁 S CTTTGAGCTGACCTGC GAGCGAGATGACCAGC 146

RESULT 40 ACD96616/ ACD96616 standard; cDNA; 130

Human colon cancer cell expressed cDNA #5028.

entry)

23-SEP-2003

YEAR ON WAR WAR WAR AND WAR AN Homo breast cancer; population genome analysis; genetic shift antibiotic resistance; antibiotic non-tolerance; congeni agriculture; food crop genome; resistance gene; retrovir 27-SEP-1999; gene; 24-OCT-2002. agriculture; foo influenza virus; sapiens reading frame detection; 99US-00406117 l crop genome; eukaryotic pa genome sequencing; cance gene; detection; shift; cancer;
ongenital disease; cancer; ome; Plasmodium;

The invention describes a method of determining

open reading frames

Page 721; 959pp; English

Example 9;

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RESULT 41
                                                     AAC1253
                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of determining open reading frames in CC the genome of organism, comprising contacting mRNA from cell of organism CC with a single oligonucleotide primer (1) at low stringency, preparing CC olNA, sequencing the product, and repeating the contacting, preparing CC olNA, sequencing the product, and repeating the contacting, preparing CC and amplifying steps with different primers and sequencing resulting CC nucleotide sequence from a genome of an organism corresponds to a nucleotide sequence of an open reading frame; for preparing a contig, CC all or part of a genome of an organism; and for sequencing CC nucleotide sequence of an open reading frame; for preparing a contig, CC all or part of a genome of an organism, and for sequencing CC nucleotide sequence of an open reading frame; for preparing a contig, CC all or part of a genome of an organism, and for sequencing CC nucleotide south which is associated with a pathological condition e.g. a colon cancer or breast cancer cell. The method is useful for analyses of CC populations of subjects and can be used to carry out genetic analyses of large or small populations more or less likely to be affilicted with the conditions of subjects and the risk of affiliction to a foetus, as well as CC the study of whether the conditions are likely to be passed to offspring through ove or sperm. The analyses for pathological conditions can be cc using this method, in the area of agriculture, for example the genomes of food crops can be conditied to determine if resistance genes are present, defects in plant CC extracted out in all animals, plants, birds, fish, etc. Using this method, in the area of agriculture, for example the genomes of food crops can be conditioned to determine if resistance genes are present, defects in plant conditions of the pathogens which may require different approaches to the rapy. This method is also applied to eukaryotic pathogens, such as cut reparations, such as conditions of pathological conditions as conditions. This
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 44
      06-OCT-2000
                                       AAC12537;
                                                                        AAC12537
                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-182626/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson AJG, Neto ED,
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                                                                                                                                                                                                                          101
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                                                                                                                                                                                                                                                                                                         Similarity
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BRENTANI R R.
                                                                        standard; cDNA; 181
                                                                                                                                                                                                                         GCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCTCATCGTCG
                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                        AGTCGGCGGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 721; 959pp;
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                           A; 44 C;
                                                                                                                                                                                                                                                                                                        16.1%;
57.9%;
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                                                                                                                                                                                       84
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                                                                        <u>В</u>Р.
                                                                                                                                                                                                                                                                                                         Score 24.8; DB 10
Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                                                                           35 G;
                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                         0 U; 0
                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an organism e.g. a huma oligonucleotide primer cDNA from mRNA of
                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                           Other;
                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                        Indels
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RESULT 42
AAC12537/c
ID AAC12
XX
AC AAC12
XX
DT 06-OC
XX
DE Humar
XX
KW Humar
KW Gene
XX
GS Homo
XX
PD 06-SI
XX
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AAC12537
                                                    EP1033401-A2
                                                                                                                                                                                                     06-OCT-2000
                                                                                                                                                                                                                                     AAC12537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                      Human
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                                                                                   sapiens
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          sequences usually correspond mainly to the 3' untranslated r of the mRNA because they are often obtained from oligo-dT pr libraries. Such ESTs are not well suited for isolating cDNA derived from the 5' ends of mRNAs and even in those cases wh cDNA sequences have been obtained, the full 5' UTR is rarely ESTs are derived from mRNAs with intact 5' ends and can ther to obtain full length cDNAs and genomic DNAs. 5' ESTs are al diagnostic, forensic, gene therapy and chromosome mapping pr They are used to obtain upstream regulatory sequences and to expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is one of a large number of 5' ESTs mRNAs encoding secreted proteins. No ORF has yet been coridentified within the present sequence. The 5' ESTs were total human RNAs or polyA+ RNAs derived from 30 different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                             181 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 16612;
                   EST;
                                                                                                                                                                                                                                                                                                       16.1%;
nilarity 67.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards
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                                                                                      (first
  expressed chromosome
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5
1 sequence
e mapping;
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mapping; ss.
                                                  EST,
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Pred.
                                                                                                                                                                                                                                                                                                                                                                            92
                                                   SEQ ID
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red. No. 5.4e
Mismatches
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                                                    NO: 16612.
                   secreted
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                  protein;
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ses where longer
rarely included. 5'
therefore be used
re also used in
ng procedures.
d to design
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prepared from
ttissues. EST
ced region (UTR)
primed cDNA
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                  cDNA isolation;
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ADS69652
ID ADS6
XX ADS6
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XX COII
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XX COII
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XX Beec
KW Becc
KW Bact
KW Bact
KW POLL
XX Zea
XX US20
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PF 06-J
XX XX 12-J
PR 112-J
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                              Stewart's bacterial Wilt; Holcus Byor, Turning infection; bacterial stripe; maize dwarf mosaic virus infection; environmental stress; water stress; pH stress; temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal dibacterial infection; Goss' Bacterial Wlit; blight; stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADS69652
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                                                                                12-MAY-1998;
21-APR-1999;
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                                                                                                                                                                      06-AUG-2001;
                                                                                                                                                                                                                               25-DEC-2003
                                (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seedling-derived polynucleotide (cpds),
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Similarity 67.3%;
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid that is a 5' expressed sequence tag (5' EST) for DNAs and genomic DNAs that correspond to 5'ESTs and for forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                      2001US-00923876
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99US-00298329.
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Pred. No. 5
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Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
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ed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spot;
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The invention relates to a corn seedling-derived polynucleotide (cdp) selected from ADS64985-ADS71316, or their complements and fragments. Also composition for the detection of altered expression of a cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a cc method of detecting a polynucleotide in a biological sample using a cdp, cc method of or using oligomers (and amplification) to recover a regulatory clement from a DNA library using oligomers designed against a cdp, a seedling specific regulatory element that regulates the expression of a cc cdp, an expression vector containing a cdp or regulatory element, a plant cransformed with the vector, a host cell containing the vector (and compounds for binding to cdp polynucleotide. TDP), an anti-CDP antibody, compounds for binding to cdp polynucleotide. The cdp polynucleotides, proteins, vectors, cells and antibodies are useful for the cd identification, evaluation and alteration of seed growth and development, consease resistance (e.g. to insect infestation, fungal disease, bacterial consease resistance (e.g. to insect infestation, fungal disease, bacterial stress, ph stress, temperature stress, pollution, injury or consect infestation of seed growth and size dwarf consease. The present segmence is cdb cDNA segmence.
                      water stress, pH stress, remperature according sequence. pesticides. The present sequence is cdp cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New corn seedling-derived polynucleotides and polypeptides, useful in identifying and altering desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ
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164 BP; 28
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 P;
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 53 C;
 38
 G;
 44 T; 0 U; 1
 Other;
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ADS69652/
ID ADS6
XX
ADS6
AC ADS6
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DT 18-N
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DE Corn
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KW Corn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 40
                                                                                                                                              seed development; disease resistance; insect inferbacterial infection; Goss' Bacterial Wlit; blight Stewart's bacterial Wilt; Holcus spot; bacterial
                                                                                                                                                                                                                                          18-NOV-2004
                                                                                                                                                                                                                                                                                             ADS69652
 06-AUG-2001; 2001US-00923876.
                                                                                                                     bacterial stripe; maize dwarf mosaic environmental stress; water stress; p
                                                                                                                                                                                                               Corn seedling-derived polynucleotide (cpds), SEQ ID 4668
                             25-DEC-2003
                                                                                                        pollution;
                                                                                                                                                                                     seedling-derived polynucleotide; cdp;
                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                            standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGACGACGATGCGGAAGCGGGATCTGGGCATCCTGCTGCTCGCCG
                                                                                                                                                                                                                                                                                                                                                                CTTCTC
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                                                                                                      injury; pesticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.4;
Pred. No. 6.
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                                                                                                                                                                       seed growth;
on; fungal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164;
                                                                                                                       re stress;
                                                                                                                                               ight; leaf spot;
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RESULT 4
AAI27481
ID AAI
XX
AC AAI
AC AAI
AC Prol
DE Prol
XX
DE Prol
XX
Prol
XX
Prol
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Prol
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OS Hom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selected from ADS64985-ADS71316, or their complements and fragments. Also cincluded are a composition for the detection of altered expression of a comp (comprising a polynucleotide selected from ADS64985-ADS71316), a cdp (comprising a polynucleotide in a biological sample using a cdp, a method of detecting a polynucleotide in a biological sample using a cdp, a cdp, a method for using oligomers (and amplification) to recover a regulatory element from a DNA library using oligomers designed against a cdp, a cdp, an expression vector containing a cdp or regulatory element, a plant cransformed with the vector, a host cell containing the vector (and compounds for binding to cdp polynucleotide. The cdp polynucleotides, compounds for binding to cdp polynucleotide. The cdp polynucleotides, containing, vectors, cells and antibodies are useful for the cdisease resistance (e.g. to insect infestation, fungal disease, bacterial conseaic virus infection) and resistance to environmental stress (e.g. water stress, ph stress, temperature stress, pollution, injury or pesticides. The present sequence is cdp cDNA sequence.
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Best Local S
Matches 40
                                                                                            Probe; human; cervical cance
                                                                                                                                     Probe
                                       WO200157278-A2
                                                                                                                                                              12-OCT-2001
                                                                                                                                                                                                                     AAI27481
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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and
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21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identifying and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                             Sequence 185
                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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2000US-0234687P.
2000US-0236359P.
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Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary
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/db_xref="taxon:32630"
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CTCCGGCCGCCG 120

TCCGGCCGCCG 120

GGTCATCTCGCT 60

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Recombinant constructs and their use in reducing gene Patent: WO 0200904-A 12 03-JAN-2002;

E. I. du Pont de Nemours and Company (US); PIONEER HI INTERNATIONAL, INC. (US)

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Nucleotide sequences of a new class o
stearcyl-acp desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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Sequence 12 from Patent
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Recombinant constructs and their use in reducing Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US); PIONE INTERNATIONAL, INC. (US)
Location/Qualifiers
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[mol_type="unassigned DNA"]
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Sequence
AX392335
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Sequence 14
AX367129
AX367129.1
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Patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemours and Company
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other sequences; artificial sequences
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Similarity 100.0%;
80; Conservative (
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                              Score 80; DB 6; Lo
Pred. No. 1.2e-05;
0; Mismatches 0;
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RESULT 10
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AUTHORS
TITLE:
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AX047784
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Best Local Similarity
Matches 80; Conserv
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                                        Query Match 19.1%;
Best Local Similarity 58.6%;
Matches 51; Conservative
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Sequence 16
AX047784
AX047784.1
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AX367129
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Recombinant constructs and their use in reducing Patent: WO 0200904-A 14 03-JAN-2002;
E. I. du Pont de Nemours and Company (US); PIONE INTERNATIONAL, INC. (US)
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences
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                                                                                                                                                           Human brain t calcium channel alpha-subunit
Patent: WO 0070044-A 16 23-NOV-2000;
The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; M
                                                                                                                                                                                                                                                                              Homo sapiens
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CGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACTCGA 89
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larity 100.0%;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"
                                                                                                                                                                                                                                        ; Metazoa; Chordata; Eutheria; Primates;
                                                                                                           organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                          Score 29.4; DB 6;
Pred. No. 4.1e+04;
D; Mismatches 36;
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Catarrhini; Hominida
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ae; Homo.
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FEATURES
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VERSION
KEYWORDS
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AUTHORS
TITLE
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Sequence 16
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Sequence 66
AR251294
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                                                                                64;
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                                                                                                                                                                                  1 (bases 1 to 197)
Lalgudi, R.V., Ito, L.Y. and Sherman, B.K.
Polynucleotides and polypeptides derived
Patent: US 6476212-A 6653 05-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain t calcium channel alpha-subunit Patent: WO 0070044-A 16 23-NOV-2000; The Johns Hopkins University (US)
Location/Qualifiers
                                                                                                                                                                                                                              Unclassified.
                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                    Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mittman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                              18.2%;
Similarity 51.2%;
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
GACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG
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                                                        GTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTC
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                                                                                                                                                                                                                                                                                                 6653
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                                                                                                                                                            Location/Qualifiers
1. .197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                   organism="unknown"
mol_type="genomic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
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58.6%;
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                                                                              Score 28; DB Pred. No. 7.6e 0; Mismatches
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Pred. No. 4.1e+04;
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                                                                              7.6e+04;
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TITLE
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RESULT 15
AFU557755
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DEFINITION
ACCESSION
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AUTHORS
TITLE
JOURNAL
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AR251294/c
LOCUS
DEFINITION
ACCESSION
VERSION
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KEYWORDS
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Aspergillus:
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AJ557755.1 (
internal trai
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Sequence 66
AR251294
AR251294.1
                                                                                                         Direct Submission
Submitted (18-APR-2003)
Universitaet Oldenburg,
                                                                                                                                                                                                                     Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; m:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 197)

1 (bases 1 to 197)

Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.

Polynucleotides and polypeptides derived

Patent: US 6476212-A 6653 05-NOV-2002;

Location/Qualifiers

1. .197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                                     Detection and identification Unpublished
                                                                                                                                               Hain, M.
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transcribed spacer
                                                                                  Location/Qualifiers
                                  /organism="Aspergillus
/mol_type="genomic DNA"
/isolate="8"
       /specific_host="Alcyonidium
/db_xref="taxon:5085"
                                                                                                                                                             1 to 191)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="unknown"
| mol_type="genomic
country="Germany:North
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                                                                                                                                                                                                                                                                                                           ITS1,
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Pred. No. 7.6e+04;
                                                                                                           Hain M.,
C. v. O.
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RESULT 17
AX393064
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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Best Local S
Matches 44
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Best Local S
Matches 44
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                   AX393064
Sequence 9
AX393064
AX393064.1
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AJ557755
AJ557755.1 GI:46406330
internal transcribed spacer 1; ITS1
Aspergillus fumi
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Homo
                                                                                                                                                                                         44; Conservative
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Submitted (18-APR-2003)
Universitaet Oldenburg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus
Aspergillus fumigatus
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                               GERMANY
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sapiens
                                                                                                                                                                                                                                                             /specific_host="Alcyonidium g
/db_xref="taxon:5085"
/country="Germany:North Sea a:
Helgoland"
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1. .191
/note="internal '
                                                                                                                                                                                                                                    1. .191
/note="internal transcribed
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                                                                                                                                                                                                                                                                                                         organism="Aspergillus"
/mol_type="genomic_DNA"
/isolate="8"
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                                        from
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                                        Patent
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Pred. No. 1.1e
0; Mismatches
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WO0206313.
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Pred. No. 1.1e+05;
0; Mismatches 28;
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1.1e+05;
hes 28;
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Strasse 9-11,
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D-26111 Oldenburg,
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AX393064/c
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Uncultured bacterium nirS g
isolate:DGGE band f2r5-ko.
AB164172
AB164172.2 GI:45421893
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AX393064
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Location/Qualifiers
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Mammalia; Eutheria;
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Patent: WO 0206313-A 9 24-JAN-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                   TCATCGTTGAGGCTCAGGTCGGATACCGCCAACTGGAACACCCTGTCGTCCTTGGCCGGC 21
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                                                                                                                      TTCTCCTCGAAGA 8
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/mol_type="unassigned DN/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Primates;
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Pred. No. 1.5e+05;
0; Mismatches 29;
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Pred. No. 1.5e+05;
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ae; Homo.
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ORGANISM

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             Shoji, T. Direct S
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On Mar 13, 2004 this sequence version replaced gi:45330784.
                                                  process using oxygen,
Unpublished
                                                                                                                                                                                                  Uncultured bacterium nirS gene isolate: DGGE band f2r5-ko.
                                                                             Microbial communities
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Unpublished
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   Submitted (26-FEB-2004)
                                                                                            Shoji,T.
                                                                                                                     Bacteria; environmental samples
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             Submission
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/codon_start=1
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/product="nitrite reductase"
/protein_id="BAD12410.2"
/db_xref="GI:45421894"
/translation="YHPEPRVASIVASHFSPEFVVNVKETGKTLMVDYSNIDALKVTE
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/country="Japan:Tokyo"
/note="PCR products amp
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/mol_type="genomic_DNA"
/isolate="DGGE band f2r5-ko"
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Pred. No. 1.4e+05;
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Tadashi Shoji,
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                                                                enhanced biological phosphorus te and nitrite as electron accep
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AX393057
AX393057.1
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Patent: WO 0206313-A 2 24-JAN-2002;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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On Mar 13, 2004 this sequence version replaced Location/Qualifiers
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                              TCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCC 119
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/transl_table=1
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/country="Japan:Tokyo"
/note="PCR products amplified
nirS3R were analyzed by DGGE"
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with wastewater"
/db_xref="taxon:77133"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/protein_id="BAD12410.2"
/db_xref="GI:45421894"
/translation="YHPEPRVASIVASHFSPEFVVNVKETGKTLMVDYSNIDALKVTE
IGSARFLHDGG"
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'isolate="DGGE band f2r5-ko"
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Pred. No. 1.4e+05;
); Mismatches 39;
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Matches 44
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Best Local Similarity
Matches 50; Conserv
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Eukaryota; Me
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Regulation of human glutamate recep Patent: WO 0206313-A 2 24-JAN-2002; Bayer Aktiengesellschaft (DE)
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                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Genset (FR)
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44; Conservative
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   CGAGATGACCAGCTCCGGCCGCCGACTCG 125
                           GCTGCGGCGGCRGTGTCGCGTTCGGCGGGATTTCTCTTCGCTCCGGCTCGGCCTAGGT
                                                   GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGACTCGACGATGAG
                                                                              17.3%;
larity 56.2%;
Conservative
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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from Patent WO0206313.
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Pred. No. 1.4e+05;
0; Mismatches 29;
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                                                                              Score 26.6; DB 6;
Pred. No. 1.4e+05;
0; Mismatches 39;
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Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates; Catarrhini; Homin
1 (bases 1 to 195)
1 (bases 1 to 195)
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 9895 02-OCT-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/9895
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC
PI JORDAN
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Mammalia; Eutheria; Primates;
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CC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,
G06F15/40
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nilarity 56.2%;
Conservative (
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JP 2001269182-A/9895
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
JORDAN
C12015/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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/mol_type="unassigned DN
/db_xref="taxon:9606"
                      Location/Qualifiers
organism="Homo
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Pred. No. 1.4e
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Catarrhini; Hominida
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Catarrhini; Hominida
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ae; Homo.
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1e; Homo.
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Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.

E Sequence tag and encoded human protein

Patent: JP 2001269182-A 9895 02-OCT-2001;

GENSET

OS Homo sapiens (human)

PN JP 2001269182-A/9895

PD 02-OCT-2001

PF 24-FEB-2000 JP 2000118773

PR 26-FEB-199 US 60/122487

PI JEAN BAPUTIST PYTT.
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Sequence tag and encoded
BD033649
BD033649.1 GI:22575391
JP 2001269182-A/9895.
Homo sapiens (human)
Homo sapiens
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nilarity 56.2%;
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JP 2001269182-A/9895
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN
                                                      19276
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                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.4e+05;
D; Mismatches 39;
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Pred. No. 1.4e+05;
); Mismatches 39;
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                                                       bp DNA
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RESULT 28
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les 49; Conserv
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1 (bases 1 to 171)

1 (bases 1 to 171)

Edwards, J.-B.D.M., Jobert, S. and Giordano, Edwards, J.-B.D.M., Jobert, S. and Giordano, EST's and encoded human proteins
EST's and encoded human proteins
Location/Qualifiers

171
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                                               Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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Sequence
AR427779
AR427779.
                                                                                                          AX988473
Sequence 191
AX988473
AX988473.1
                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 171)
Edwards, J.-B.D.M., Jobert, S. and
EST's and encoded human proteins
Patent: US 6639063-A 19276 28-OCT
Location/Qualifiers
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Dumas Milne Edwards, J.B., Jobert ESTs and encoded human proteins Patent: EP 1104808-A 19276 06-JI
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/mol_type="genomic
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                                                                                                           GI:40994650
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n patent US
                                               Chordata;
Primates;
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Pred. No. 1.7e+05;
L; Mismatches 39;
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Pred. No. 1.7e+05;
l; Mismatches 39
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t EP1104808.
                      Jobert, S. and Giordano
   06-JUN-2001;
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                                                Craniata; Vo
Catarrhini;
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                                            ertebrata; Euteleostomi; Hominidae; Homo.
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RESULT 31
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                                                                                    ORGANISM
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Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Primates; C:
1 (bases 1 to 171)
Edwards, J.B.D.M., Jobert, S. and
EST and encoded human protein
Patent: JP 2002010789-A 15409 1
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Sequence 19276 :
AX988473
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Homo sapiens
Eukaryota; Me
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                                                                                 BD123332.1 GI:23218277
JP 2002010789-A/15409.
Homo sapiens (human)
Homo sapiens
                                                                                                                                       BD123332
EST and encoded human
BD123332
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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55.1%;
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Pred. No. 1.7e+05;
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Pred. No. 1.7e+05;
L; Mismatches 39;
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                           and Giordano, J.
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                                                      Craniata; Ve Catarrhini;
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                                                                  Vertebrata;
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                                                                   Euteleostomi;
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C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68,
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JP 2002010789-A/15409
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
                                                                                                                                                                                                                           EST and encoded human protein
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                   /organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 1.7e+05;
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ae; Homo.
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Sequence 98:
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CQ424819.1
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Location/Qualifiers
                                                                   Novel genes, compositions, kits, and me assessment, prevention, and therapy of Patent: WO 0151628-A 9853 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
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CQ424819
Sequence 9853 from Patent
CQ424819
CQ424819.1 GI:41377048
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                                                                                                                                            Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
                                                                                                                                                                            Mammalia;
                                                                                                                                                                                          Eukaryota;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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larity 55.1%;
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/db_xref="taxon:9606"
            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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RESULT: 35
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Sequence 19:
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                                                Lillie, J., Xu, Y., Wang, Y. and Steinmann, K. Novel genes, compositions, kits, and methods fassessment, prevention, and therapy of breast Patent: WO 0151628-A 1955 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)
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Mammalia; Eutheria; Primates;
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Pred. No. 1.8e+05;
); Mismatches 40
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Pred. No. 1.9e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chrzavzez, E.E. and Aufrere, R.
METHOD FOR DETECTING HEAT-RESISTANT MI
CONTAMINATING CERTAIN FOOD PRODUCTS
PAtent: WO 9638587-A 3 05-DEC-1996;
ULTRA PROPRE NUTRITION IND REC (FR)
Other publication FR 2734844 961206.
Location/Qualifiers
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                                             METHOD FOR DETECTING HEAT-RESISTANT CONTAMINATING CERTAIN FOOD PRODUCTS Patent: WO 9638587-A 3 05-DEC-1996; ULTRA PROPRE NUTRITION IND REC (FR) Other publication FR 2734844 961206.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
 organism="unidentified"
|
| mol_type="unassigned DN
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Pred. No. 1.8e+05;
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Sequence 3
AR110714
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Sequence
AR110714
                                                                               1 (bases 1 to 183)
Chrzavzez nee Taddei, E. and Aufrere, Method for detecting heat-resistant contaminating certain food products Patent: US 6117636-A 3 12-SEP-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 183)
Chrzavzez nee Taddei, E. and Aufrere,
Method for detecting heat-resistant
contaminating certain food products
Patent: US 6117636-A 3 12-SEP-2000;
Location/Qualifiers
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Unclassified.
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                                             /organism="unknown"
/mol_type="unassigned
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/mol_type="unassigned
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Apteronotus leptorhynchus
Apteronotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Er
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apteronotidae; Apteronotus.
1 (bases 1 to 105)
Dimmick, W.W. and Larson, A.
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8812312
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Dimmick, W.W. and Larson, A.
Direct Submission
Submitted (10-AUG-1995) University
Boulevard, Lawrence, KS 66045, USA
                                                                                                                 ALU33657 1
Apteronotus leptorhynchus
U33657
U33657.1 GI:2443919
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Apteronotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apteronotidae; Apteronotus.
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Dimmick, W.W. and Larson, A.
A molecular and morphological perspective on relationships of the otophysan fishes
Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)
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AB164173.1
                                                                                                                                                                                                           Submitted (26-FEB-2004) Tadashi Shoji, The L
Department of Urban Engineering; 7-3-1, Hong
113-8656, Japan (E-mail:shoji@env.t.u-tokyo.
Tel:81-3-5841-7784, Fax:81-3-5841-8538)
                                                                                                                                                                                                                                                                                                         Microbial communities process using oxygen, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB164173
Uncultured bacterium nirS isolate:DGGE band f2r5-sa.
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Dimmick, W.W. and Larson, A.
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                                                                                           /organism="uncultured bacterium"
/mol type="genomic DNA"
/isolate="DGGE band f2r5-sa"
/isolation_source="activated sludg
with wastewater"
/db_xref="taxon:77133"
/gene="nirs" <1. .>165
                                       /note="PCR products amplified nirS3R were analyzed by DGGE"
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/db_xref="taxon:36674"
/tissue_type="muscle"
/note="AC28S4"
                                                                    country="Japan:Tokyo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-FEB-2004) Tadashi Shoji, The University of Tokyo, Department of Urban Engineering; 7-3-1, Hongo, Bunkyo, Tokyo 113-8656, Japan (E-mail:shoji@env.t.u-tokyo.ac.jp, Tel:81-3-5841-7784, Fax:81-3-5841-8538)

Location/Qualifiers
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Unpublished
2 (bases 1 to 165)
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/transI_table=11
/transI_table=11
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/protein_id="BAD12411.1"
/db_xref="GI:45330787"
/translation="YHPEPRVASIVASHYKPEFVVNVKETGQTLLVDYSNVDALKVTTIGTARFLHDGG"
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/protein_id="BAD12411.1"
/db_xref="GI:45330787"
/translation="YHPEPRVASIVASHYKPEFVVNVKETGQTLLVDYSNVDALKVTTIGTARFLHDGG"
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/mol_type="genomic DNA"
/isolate="DGGE band f2r5-sa"
/isolation_source="activated sludge
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/country="Japan:Tokyo"
/note="PCR products amplified
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/product="nitrite
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Score 25.4; DB 1;
Pred. No. 2.4e+05;
0; Mismatches 31;
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Pred. No. 2.4e+05;
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Mammalia; Eutheria; Primates; Catarrhini; Hominida

ENCE 1 (bases 1 to 123)

HORS Szostak, J.W., Roberts, R.W. and Liu, R.

Sorting of proteins using RNA-protein fused body

MAL Patent: JP 2002536025-A 29 29-OCT-2002;

THE GENERAL HOSPITAL CORP

OS Homo sapiens (human)

PN JP 2002536025-A/29

PD 29-OCT-2002

PF 01-FEB-2000 JP 2000598669

PR 09-FEB-1999 US 09/247190

PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU

PC C12N15/09, C07K7/00, C07K14/00, C12Q1/68, C12N15/00

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Spencer, D.H.,
                         Pseudomonas aeruginosa
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Class: shotgun.
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Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Fax: 2066857244
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'clone="pacs2-164_6657"
'clone_lib="pacs2-164"
'note="clinical isolate 2-164 Whole
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mol_type="genomic DNA'
strain="2-164"
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Triticum aestivum (bread wheat)
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Box 352145, Seattle, WA:
Tel: 2062216954
Fax: 2066857244
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                                                                                                                                                               This sequence has been
                                                                                                                                                                               Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                             Genoplante, a major 
Unpublished (2003)
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophy Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooideae; Triticeae; Triticum.
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http://genoplante-info.infobiogen.fr)
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/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole library."
                         /tissue_type="grain
pollination)"
                                                   'db_xref="taxon:4565"
'clone="GR45114C04"
                                                                           organism="Triticum aestivum"
/mol_type="mRNA"
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/clone="GR45114C04"
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/cultivar="recital"
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Ma,L., Wangc,J., Chen,C., Liu,X., S
Jiao,Y., Sun,N., Zhang,X., Bao,J.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional reguits comparison to Arabidopsis
                                                                           Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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Jiao,Y., Sun,N., Zhang,X., Bao,J.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regults comparison to Arabidopsis
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Chinese Academy of Sciences, I
Tel: 86-10-80481559
Fax: 86-10-80488676
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Rice genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chen Chen
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa E
/note="Oryza sativa exon t
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Be
Tel: 86-10-80481559
Fax: 86-10-80488676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NN1155-271000-628-a09&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Ro
                                                                                                                                                                                                                                                                                  Shotgun sequencing of
                                                                                                                                                                                                                                                                                                    Simpson, A.J
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                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
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(mol_type="genomic DNA"
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/clone_lib="Oryza sativa Express Library"
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Seq primer: puc 18 forward
Sequence was derived from the FAPESP/LICR Human Cancer Genome Project Interval Interval
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida, Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.Brunstein,A., deOliveira,P.S., Bucher,P., Jongenee
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                    ocation/Qualifiers
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3.S., Simpson,D.H.,
sel,C.V.,
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/clone lib="NNN1155"
/clone lib="NNN1155"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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/cultivar="recital"
/db_xref="taxon:4565"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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BOMOF14TF BO 2_3_KB Brassica o
genomic survey sequence.
BZ509933
BZ509933.1 GI:27033989
GSS.
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Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid p:
Seq primer: TF
Class: sheared ends.
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1 (bases 1 to 653)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                  Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                     9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun sequencing Unpublished (2001)
Other GSSs: BOMQF14TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
Brassica oleracea
                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
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ilarity 55.6%;
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                                                                Location/Qualifiers
1. .653
organism="Brassica"
| mol_type="genomic D
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/clone lib="BO 2 3 KB"
/clone lib="BO 2 3 KB"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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me shotgun sequencing of Brassica oleracea
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0; Mismatches
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Best Local Similarity
Matches 70; Conserv
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odg84c07.g1
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                                                                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg84 row: c column: 07
Seq primer: -28RPpOT reverse
Class: shotgun
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BH925906
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Delehaunty,K., Fewell,G., Fulton,L., McCc
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica
Unpublished (2002)
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Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Richard K. Wilson
                                                                      Similarity
CTCGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG 77
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Location/Qualifiers
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                                                                                                                                      /mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone_lib="B.oleracea002"

/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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/db_xref="taxon:3712"
/clone="BOMQF14"
/clone="BOMQF14"
/clone="BO_2 3 KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_DHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                               organism="Brassica oleracea"
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B.oleracea002 Brassica
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                                                    Score 36.4; D. Pred. No. 34; O; Mismatches
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вн925906.1
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg84 row: c column: 07
Seq primer: -28RPpOT reverse
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delehaunty, K., Fewell, G., Fulton, L., McCNash, W., Rabinowicz, P.D. and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun reads from Brassica Unpublished (2002)
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the DNA was provided by Pablo Rabinowicz (CSHL) and the
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Pred. No. 34;
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AUTHORS
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Local Similarity
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Unpublished (2001)
Other_GSSs: BONJT45TF
Contact: Chris Town
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BONJT45TR BO_1.6_2_KB_tot
genomic_survey sequence.
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BZ427562
BZ427562.1
Whole genome shotgun sequencing Unpublished (2001)
Other_GSSs: BONJT45TF
Contact: Chris Town
TIGR
                                                                                                                   Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta

Spermatophyta; Magnoliophyta; eudicotyledons; core

rosids; eurosids II; Brassicales; Brassicaceae; B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Roc
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracl Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 818)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.
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                                                                                       1 (bases 1 to 818)
Town, C.D., Van Aken, S.,
                                                                                                                                                                                                     Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                                                                                                                                                                          416
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/note="Vector: pHOS1; Site_1:
total DNA inserted into pHOS1
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="BONJT45"
                                                                                                                                                                                                                                          GI:26669268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36.4;
Pred. No. 34;
                                                                                           Utterback, T.
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Brassica olera
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ore eudicots;
Brassica.
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                                                                                        Fraser,C.M.
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RESULT 17
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CL980758
CL980758.1 GI:52416004
GSS.
Cryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.
1 (bases 1 to 834)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                  Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing
Tel: 86-10-80481559
Fax: 86-10-80488676
                                                                                                                                                                                                                                                                                     Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome its comparison to Arabidopsis
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL980758 834 bp DNA linear GS: OSIFCC045376 Oryza sativa Express Library Oryza sativa
                                                                                                                                                                    Email: chenchen@genomics.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-3523
Fax: 301-838-0208
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is from a doubled haploid
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/note="Vector: pHOS1; Site_1:
total DNA inserted into pHOS1
                                            organism="Oryza sativa (indica mol_type="genomic DNA" db_xref="taxon:39946"
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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using BstXI linkers"
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Be
Tel: 86-10-80481559
Fax: 86-10-80488676
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa E
/note="Oryza sativa exon t
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Direct Submission

Direct Submission

L Submitted (12-APR-2000) Genoscope - Centre National de :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genos/
- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as par scale clone-end sequencing project of the Tetraodon nic genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                            Tetraodon
041B18 of
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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Bradyrhizobium japonicum
Bacteria; Proteobacteria;
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This sequence is a single read and was generated scale clone-end sequencing project of the Tetraod genome. For more information, please take a look http://www.genoscope.cns.fr/Tetraodon.
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Direct Submission

Direct Submitted (12-APR-2000) Genoscope - Centre

BP 191 91006 EVRY cedex - FRANCE (E-mail :

- Web : www.genoscope.cns.fr)
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                         Bradyrhizobiaceae; Bradyrhizobium.
1 (bases 1 to 787)
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="041B18"
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Tel: 864 656 7288
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Bradyrhizobiaceae; Bradyrhizobium.

1 (bases 1 to 787)

Tomkins, J.P., Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A. Gonzechea, J.L., Stacey, G., Sadowsky, M.J. and Wing, R.A. and Marker-dense, sequence-ready map of the Bradyrhizobium
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Clemson University
100 Jordan Hall, Clemson, SO
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Class: BAC ends
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Contact: Wing RA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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Fax: 864 656 4293
                                                                                                                                             Email: rwir
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/mol_type="genomic DNA"
/strain="USDA110"
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/note="Vector: pIndigo536; Site_1: Hi
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lab_host="E. coli"
organism="Bradyrhizobium"
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Submitted (12-APR-2000) Genoscope - Centre N
BP 191 91006 EVRY cedex - FRANCE (E-mail : s
- Web : www.genoscope.cns.fr)
This sequence is a single read and was gener
scale clone-end sequencing project of the Te
genome. For more information, please take a
http://www.genoscope.cns.fr/Tetraodon.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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/lab_host="E. coli"
/clone_lib="B. japonicum BAC library"
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                            /organism="Tetraodon nigroviridis"
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@genoscope.cns.fr
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
/clone="063118"
                                                                                                                                                                                          organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
                                                                                                                            'note="Genoscope
                                                                                                                                              clone
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library G from Tetraodon
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Pred. No. 38;
                                                              Score 36.2;
Pred. No. 38;
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nigroviridis
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzaa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anam-Dong, Seongbuk-Gu,
Tel: +82 2 3290 3005
Fax: +82 2 3290 3501
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Contact: Seo YW
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Korea University
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                                                                                                                                                                                                                                                                                                     Conservative
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          5MT resistant rice mutant
                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="5MT treated leaves, stems, and roots"
/dev_stage="seedling grown for 3 weeks"
/lab_host="XL1-Blue MRF'"
/clone_lib="5MT resistant rice mutant cDNA library"
/note="Vector: pBluescripts SK(+/-) phagemid; The rice
mutant resistant to growth inhibition by 5MT were selected
from the callus irradiated with gamma ray of 50 Gy through
rice cv. Donganbyeo embryo culture.For construction of the
cDNA library, 5MT resistant homologous rice mutants were
treated by 5MT for 3 weeks."
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|mol_type="mRNA"
|cultivar="Donganbyeo"
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erization of
ltryptophan (5MT)
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Poaceae;
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RESULT 27
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sequence.
AL306353
AL306353.1 GI:8204690
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Tetraodon
013I12 of
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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CO435934
CO435934.1 GI:53552954
EST.
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Tel: +82 2 3290 3005
Fax: +82 2 3290 3501
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Department of Crop
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1 (bases 1 to
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Location/Qualifiers
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/tissue_type="5MT treated leaves, stems, and roots"
/dev_stage="seedling grown for 3 weeks"
/lab_host="XL1-Blue MRF'"
/clone_lib="5MT resistant rice mutant cDNA library"
/note="Vector: pBluescripts SK(+/-) phagemid; The rice
mutant resistant to growth inhibition by 5MT were selected
from the callus irradiated with gamma ray of 50 Gy.through
rice cv. Donganbyeo embryo culture.For construction of the
cDNA library, 5MT resistant homologous rice mutants were
treated by 5MT for 3 weeks."
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(mol_type="mRNA"

/cultivar="Donganbyeo"
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library A from Tetraodon
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survey sequence T3 end of clone
nodon nigroviridis, genomic survey
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Submitted (12-APR-2000) Genoscope - Centre National of Submitted (12-APR-2000) Genoscope - Centre Nati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fizames, C., Fischer, C., Bouneau, L., Billault, A., (Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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Estimate of human gene number provided by genome-wusing Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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013I12 of
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                             sequence.
AL306353
AL306353.1 GI:8204690
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="013I12"
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@genoscope.cns.fr
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Direct Submission

Birect Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a larg

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.
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Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie, Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R. Development of Barley Transcriptome Resources Unpublished (2001)
Contact: Waugh R, Marshall DF
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                       Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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EBro08_SQ010_K07_R root, 3 week,
Hordeum vulgare subsp. vulgare ci
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                                                           est@scri.sari.ac.uk.
                                        Location/Qualifiers
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/db_xref="taxon:99883"
/clone="013112"
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mol_type="genomic DNA"
  organism="Hordeum vulgare
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Hordeum vulgare subsp. vulgare
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Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                              Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
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                                                                                                                                                                                                                                                                                                               Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudi
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,
Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ767987
                                                                                                                                                                                                                                                                                                   Contact: Waugh R, Marshall DF
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/db_xref="taxon:112509"
/clone="EBro08_SQ010_K07"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, d
            /mol type="mRNA"
/cultivar="Optic"
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/db_xref="taxon:112509"
/clone="EBro08_SQ010_K07"
/tissue_type="root"
/dev_stage="3_week"
/lab_host="DH108"
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                                                                                                                                                                                Location/Qualifiers
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'cultivar="Optic"
                                                                                                                                                 organism="Hordeum vulgare subsp. vulgar
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RESULT 31
CE011375
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AUTHORS
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Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 397)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003) 22875432
                                                                                                                                                                                                                                                                                                                                       Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
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89
                                                                                                                                                                                                                                                                                                            Tel: 301-838-0200
Fax: 301-838-0208
                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
                                                                                                                                     /clone_lib="Dog_Library"
/note="Site_1: BstXI; Libraries were prepared
peripheral_blood"
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                                                                                                                                                                                 /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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0; Mismatches
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Pred. No. 55;
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The Institute for Genomic R
Department of Eukaryotic Ge
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
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1 (bases 1 to 397)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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Class: shotgun.
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/note="Site 1: BstXI; Libraries
peripheral blood"
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/mol_type="genomic DNA"
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/strain="Standard Poodle"
/db_xref="taxon:9615"
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Pred. No. 55;
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var-group) cDNA
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RESULT 34
CB682412/c
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Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Pcd 77
          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 624)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Contact: Rod Wing
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CB682412
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 624)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur. E.
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EST.
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BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
Seq primer: gta aaa cga cgg cca gtg.
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Tel: 520 626 3967
Fax: 520 621 9288
Fax: http://genome.arizona.edu
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/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEf"
/note="Vector: pBluescript I
XhoI; Uninfected Control"
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf09L11"
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                                                                                                                                                 Centro de Biologia Molecular e Engenharia
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq
                                                       Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                      Vettore,A.L., da Silva,F.R., Kemper,E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                               Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Saccharum; Sacc
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SCCCST3C12B03.g ST3
5', mRNA sequence.
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Saccharum officinarum
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Fax: 520 621 9288

Email: http://genome.arizona.edu
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Plate: 09 row: L column: 11
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Biological Sciences West,
85721-0088, USA
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf09L11"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEf"
/note="Vector: pBluescript I
xhoi; Uninfected Control"
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organism="Saccharum"
/mol_type="mRNA"
                                             Location/Qualifiers
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les; Poaceae; PACCAD
Saccharum officinarum
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CC) at
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AUTHORS
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CA198784/c
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Matches 80
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EST.
Saccharum officinarum
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                                                                                                                                                          Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Paccharum officinarum
                                                                                                                                                                                                                                                                                                             Centro de Biologia Molecular e Engenharia
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                     Vettore,A.L., da Silva,F.R., Ke
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7
Contact: Arruda P
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SCCCST3C12B03.g
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80; Conservative
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/clone lib="ST3"
/clone lib="ST3"
/note="Organ: Fourth apical stalk internodes of adult /note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: Sall; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at the internal columns.
                                                            /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCCST3C12B03"
'note="Organ:
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                   lab_host="DH10B"
clone_lib="ST3"
                                                                                                                           organism="Saccharum officinarum"
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Pred. No. 54;
Fourth apical stalk internodes
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EcoRI; Site_2:

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KEYWORDS
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AI399069
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

1 (bases 1 to 590)
Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P.L.,
Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, E.,
Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K.,
Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S.,
Trujillo, R., Valentine, J., Wells, A., Werner-Washburne, M., Yazzie, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80;
                                                                                                                                                                                                                                                                                                                                                                                         Email: ngp@biology.unm.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biology
University of New Mexico
Castetter Hall, Albuquero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Natvig, D.O./Nelson, M. Department of Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa
Fungal Genet. Biol.
97435549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trujillo, R., Va and Natvig, D.O.
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NCW01B11T3 Westergaards
mRNA sequence.
AI399069
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 505 277 3411
Fax: 505 277 0304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequences from conidial, mycelial, and
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                                                                                                                                                                                 /db_xref="taxon:5141"
/clone="W01B11"
/clone_lib="Westergaards"
/note="Vector: pBlueScript
                                                                /sex="Mating type A"
/tissue_type="Unfertilized sexual tissue"
/dev_stage="Unfertilized sexual stage"
/lab_host="E. coli"
                                                                                                                                                                                                                                                              organism="Neurospora"

(mol_type="mRNA"

/strain="74-OR23-IV A
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0; Mismatches
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Best Local S
Matches 63
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MEDLINE
PUBMED
                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                      Contact: Natvig, D.O./Nelson, M.A.
Department of Biology
University of New Mexico
Castetter Hall, Albuquerque, NM 8.
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nelson, M.A., Kang, S., Braun, E.L., Crawford, M.E., Dolan, P. Leonard, P.M., Mitchell, J., Armijo, A.M., Bean, L., Blueyes, Cushing, T., Errett, A., Fleharty, M., Gorman, M., Judson, K., Miller, R., Ortega, J., Pavlova, I., Perea, J., Todisco, S., Trujillo, R., Valentine, J., Wells, A., Werner-Washburne, M., and Natvig, D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
1 (bases 1 to 590)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequences from conidial, mycelial, Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
97435549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AI399069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI399069
NCW01B11T3 Westergaards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora
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                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGCTCATCGTCGAGTCGGCGGCCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCGGTTACCANTACCAGTCTCATACTCAGCCCCAGCCGGACAGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                              /sex="Mating type A"
/tissue_type="Unfertilized sexual tissue"
/dev_stage="Unfertilized sexual stage"
/lab_host="E. coli"
/clone_lib="Westergaards"
/note="Vector: pBlueScript SK (-); Site_l: EcoRI; Site
XhoI; Westergaard's medium (Nitrogen limiting). Floati
mycelial mats grown at 25C for 36 hours. cDNA
directionally cloned into pBluescript SK(-) using the
Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
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                                                                                                                                                                                                                                                                   /organism="Neurospora crassa
/mol_type="mRNA"
/strain="74-OR23-IV A (FGSC
/db_xref="taxon:5141"
                                                                                                                                                                                                                                                         /clone="W01B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crassa
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Pred. No. 61;
O; Mismatches
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0
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                                                                                                                                                                                                                                                                                                                          crassa"
                  61;
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Crassa
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                                                                                                                                 SK (-); Site_1: BcoRI; Site (Nitrogen limiting). Floating
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Neurospora.
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Blueyes, E.,
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e W01B11
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RESULT 39
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AUTHORS
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Best Local S
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centro de Biologia Molecular e Engenharia Ge Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, B Tel: 55 19 3788 1137

Pax: 55 19 3788 1089

Email: parruda@unicamp.br
Clone distribution: clone distribution infor through the Brazilian Clone Collection Cente http://www.bcccenter.fcav.unesp.br
Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.
Location/Qualifiers
   122
                                               324
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CA227997
CA227997.1
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                                                                                                                                                                                                                   78;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Saccharum; Sac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA227997
704 bp mRNA linear EST 25-SEP-2003 SCJLFL3015B05.b Saccharum officinarum FL3 Saccharum officinarum CDNA clone SCJLFL3015B05 3', mRNA sequence.
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                                               GCCGACCAGCCAGGGGCCTCCTTCACAACGTCGAGCGAGATGTCCATCTCGGCGACCCTC 383
                                                                                       ATCGTCGAGTCGGCCGGCCGACTCGACGATGAGCGAGATGACCAG
                                                                                                                                 GGCCTCTCCTGAGGCTGAGGCCCGGCGACGGGCGGGGGCTGGCACGCT
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   CTCGACGATGAGCGAGATGACCAGCTCCG 150
                                                                                                                                                                       GGCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGGAGCT
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                                                                                                                                                                                                                23.0%;
llarity 52.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/clone lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
/note="Organ: Base of developing inflorescence (5cm-long);
Vector: pSport1; Site 1: SalI; Site 2: NotI; An
unidirectional cDNA library generated from [Base of
developing inflorescence (5cm-long)]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
                                                                                                                                                                                                                                                                                                                        http://sucest.lad.ic.unicamp.br/public"
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/db_xref="taxon:4547"
/clone="SCJLFL3015B05"
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No. 61;
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les; Poaceae; PACCAD
Saccharum officinarum
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Clone distribution: clone distribution ir
through the Brazilian Clone Collection Ce
http://www.bcccenter.fcav.unesp.br
Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 75; Conserv
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Centro de Biologia Molecular e Engenharia
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
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Vettore, A.L., da Silva, F.R., Kemper, E.L.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    704 bp mRNA linear SCJLFL3015B05.b Saccharum officinarum FL3 Saccharum cDNA clone SCJLFL3015B05 3', mRNA sequence. CA227997
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Saccharum officinarum
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GCCTCAGCCTCAGGAGAGGCC
                                                              GCGAGATGACCAGCTCCGGCC 153
                                                                                                                               GCCTGCACAGCGCGCAATGCCTCAGTGCG
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/note="Organ: Base of developing inflorescence (5cm-long);
Vector: pSport1; Site 1: Sall; Site 2: NotI; An
unidirectional cDNA library generated from [Base of
developing inflorescence (5cm-long)]. cDNA was prepared
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(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
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/db_xref="taxon:4547"
/clone="SCULFL3015B05"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.4; | Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Center (BCCC)
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RESULT

41

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LOCUS
DEFINITION
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BF483067/c
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Best Local
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                                    WHE2314_D05_G1
aestivum cDNA
BF483067
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                                                                                                                                                                                                                                                                                                                                                                              53;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 441)
1 (bases 1 to 441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequence have been trimmed to remo
quality sequence with phred score
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="WHE2314 D05 G10"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
cultivar="Chinese S;
db_xref="taxon:4565
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                                                   G10ZS Wheat pre-anthesis spike cDNA
A clone WHE2314_D05_G10, mRNA sequer
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                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB Pred. No. 78; 0; Mismatches
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                                                                        linear EST 06-DEC-2000 cDNA library Triticum
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Poaceae;
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BQ805125
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                                                                                                                                                                                                                                                                                                                                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                    BQ805125 571 bp mRNA WHE3563_B09_C17ZS Wheat developing grains aestivum cDNA clone WHE3563_B09_C17, mRNA BQ805125 GI:22029334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer: Stratagene SK primer.
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
                                                            Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 Buchanan Street,
Tel: 5105595773
Fax: 5105595818
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                                             Pooideae;
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(bases 1 to
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="WHE2314_D05_G10"
/tissue_type="Spike_before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
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                                         Triticeae; Triticum.
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Anderson, O.D., Chao, S.,
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 Chin, A.,
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 Close, T.J.,
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                                                                                                                                                                                                                                                                                                                                                                     Local
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US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595818
BQ805125
WHE3563_B09_C17ZS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequences have been trimmed
quality sequence with phred
Seq primer: SK primer.
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                                                                                                                                                                                                                                                                                                                                              Similarity 63.9
63; Conservative
                                                                                                                                                                                                                                                                                             CGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACT 86
                                                                                                                                                    CGGCCAGGGGCGACGGCAACGGC
                                                                                                                                                                                              CGACGATGAGCGAGATGACCAGC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="wheat developing grains cDNA library"
/clone lib="wheat developing grains cDNA library"
/note="vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
240C/170C day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240C/170C day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 370C/170C day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 370C/170C
day/night plus drought, without post-anthesis fertilizer,
environment 5) 370C/170C day/night plus drought, with
post-anthesis fertilizer, Environment 6) 370C/170C
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
cDNA library was made using poly (A) RNA, and the cDNA
clones were in vivo excised to give pBluescript SK(-)
phagemids in the TJ Close lab (Chin, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA gennencing were performed in the OD
                                                                                                                                                                                                                                                 CGAGGCGGCGCCGTCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="WHE3563_B09_C17"
/tissue_type="whole grains"
/dev_stage="3-44_days_post a
/lab_host="E._coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cultivar="Butte 86"
db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                            Score 35; DB Pred. No. 77; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and DNA sequencing were (others)."
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brary Triticum
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46 GCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGAC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.

The structure and function of the expressed portion of the genomes - Developing grains cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aestivum cDNA clone WHE3563_B09_C17, mRNA sequence.
BQ805125
BQ805125.1 GI:22029334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: oandersn@pw.usda.gov
Sequences have been trimmed
quality sequence with phred
Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomes - Developing grains 
Unpublished (2002)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum
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                                                                                                                              Similarity
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st Area, Western Regional Research Center
D Buchanan Street, Albany, CA 94710, USA
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                                                                                               22.7%;
larity 63.9%;
Conservative
                                                                                                                                                                                                                                                                 well-watered, without post-anthesis fertilizer, Environment 3) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170C day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370C/170C day/night plus drought, with post-anthesis fertilizer, Environment 5) 370C/170C day/night plus drought, with post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
/clone="WHE3563_B09_C17"
/tissue_type="whole_grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="Wheat developing grains cDNA library"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
240C/17oC day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240C/17oC day/night,
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Location/Qualifiers
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cultivar="Butte 86"
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Kupfer, D., Lai, H., Nelson, M. and Roe, B.

ESTS from a Neurospora crassa Sexual cDNA Library

Unpublished (2001)

Other_ESTs: blf04np.fl

Contact: Bruce A. Roe, University of Oklahoma, broe@

Contact: Bruce A. Roe, University of Oklahoma, broe@

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Chemistry

Advanced Center for Genome Technology, University of Chemistry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact Dr. Mary Anne Nelson, Department on New Mexico, Albuquerque, NM 87131 (e-mail regarding clone availability Seq primer: M13 Universal Reverse Primer High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620 Parrington Oval, Norman, Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; Ascomycota;
Sordariomycetidae; Sordariale;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora
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                                                                                                                                                                                                                       CTCATCGGCCAGAAGCCCGCCCAACAGCCTCCTCGCTCGTCTCCAGGGCGCCCCG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of
pBluescript; 3' end of cDNA cloned into XhoI site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBluescript;
pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Neurospora
vector system"
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/dev_stage="sexual"
/lab_host="E. coli strain SOLR"
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mol_type="mRNA"
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db_xref="taxon:5141"
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Pred. No. 87;
O; Mismatches
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Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                        430;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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US-09-987-194A-14
US-10-981-293-24
US-10-981-293-24
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RESULT 2
US-09-887-194A-13/c
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Glassman, Kimberly F.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Kinney, Anthony

APPLICANT: Lowe, Keith S.

APPLICANT: Nichols, Scott E.

APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND

FILE REFERENCE: BB1449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO 13

LENGTH: 154

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
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US-09-812-350-39
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VS-10-282-122A-26073
VS-10-282-122A-11328
VS-10-282-122A-11328
VS-10-282-122A-11328
VS-10-282-122A-11328
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US-10-437-963-60837
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US-10-437-963-100458
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Pred. No. 2.2e-37;
; Mismatches 0;
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Sequence 37821, A
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Sequence 26073, A
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Sequence 11328, A
Sequence 11328, A
Sequence 60837, A
Sequence 60837, A
Sequence 157, App
Sequence 157, App
Sequence 100458,
Sequence 100458,
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Sequence 25, Application US/09934900

Publication No. US20030054521A1

GENERAL INFORMATION:

APPLICANT: Booth, Russ

APPLICANT: Cahoon, Rebecca E

APPLICANT: Hitz, William D

APPLICANT: Yadav, Naren

TITLE OF INVENTION: Nucleotide Sequences of

TITLE OF INVENTION: ACP Desaturase

FILE REFERENCE: BB1476 US NA

CURRENT APPLICATION NUMBER: US/09/934,900

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/22696

PRIOR APPLICATION NUMBER: 60/22696

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

SEQ ID NO 25

LENGTH: 154

TYPE: DNA

CRGANISM: Artificial Sequence
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US-09-934-900-25
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APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:
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; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: region of pKS133
US-09-887-194A-13
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Publication No.
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LENGTH: 154
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                                                                                                                            APPLICANT: McGonigle, Brian
TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide Sequences
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
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                                  ORGANISM: Artificial Sequence
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  OTHER INFORMATION:
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les 154; Conservative
                                                                                                                                                                                                                                                                                                                            INFORMATION:
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Yadav, Naren
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Hitz, William D
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100.0%; Pred. No. 2.2e-37;
tive 0; Mismatches 0;
sequence containing a NotI site flanked
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; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
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US-10-734-947-7/c
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Best Local S
Matches 154
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SOFTWARE: Microsoft Off:
SEQ ID NO 7
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Best Local
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                                                    APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rel
APPLICANT: Hitz, Will
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TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO OF
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
                                   APPLICANT:
 APPLICANT:
TITLE OF I
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TYPE: DNA
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INVENTION: Nucleotide Sequences
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                                              Cahoon, Rebecca
Hitz, William D
               Kinney, Anthony
Yadav, Naren
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Pred. No. 2.2e-37;
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US-10-981-293-25/c
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                                                                     Matches
                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                    SOFTWARE: Microsoft Office
SEQ ID NO 25
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Applica Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Cahoon, Re
APPLICANT: Hitz, Will
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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ENGTH: 154
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Similarity 100.0%;
54; Conservative 0;
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   CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGG
                             CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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                                                                                                                                                   Description of Artificial Sequence: region of pKS133
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                                                                 Score 154; DB 19;
Pred. No. 2.2e-37;
; Mismatches 0;
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Pred. No. 2.2e-37;
Mismatches 0;
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RESULT 10
US-10-459-159-1/c
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                                                                                      APPLICANT: McGonigle, Brian
APPLICANT: Odell, Joan T.
TITLE OF INVENTION: METHOD TO INCREASE THE IS
TITLE OF INVENTION: PRODUCING INCREASED LEVE
FILE REFERENCE: BB1526 US NA
CURRENT APPLICATION NUMBER: US/10/459,159
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 60/388,280
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 10
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APPLICANT: Odell, Joan T.
TITLE OF INVENTION: METHOD TO INCREASE THE I
TITLE OF INVENTION: PRODUCING INCREASED LEV
FILE REFERENCE: BB1526 US NA
CURRENT APPLICATION NUMBER: US/10/459,159
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 60/388,280
PRIOR FILING DATE: 2002-06-13
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Best Local S
Matches 154
                   SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 7701
TYPE: DNA
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Publication No. US20
GENERAL INFORMATION
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SOFTWARE: Microsoft Offic
SEQ ID NO 1
LENGTH: 7701
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LOCATION: (6516)..(6516)
OTHER INFORMATION: n = A
ORGANISM: expression vector pKS151
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ORGANISM: expression
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Pred. No. 1.8e-37;
; Mismatches 0;
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RESULT 12
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APPLICANT: Maxwell, Carl A.
APPLICANT: Hession, Aideen O.
TITLE OF INVENTION: TRANSGENIC PLANTS WITH A
FILE REFERENCE: BB1523 US NA
CURRENT APPLICATION NUMBER: US/10/427,570A
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 9
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SEQ ID NO 9
LENGTH: 77
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Best Local S
Matches 154
Sequence 9, Application US/10427570A Publication No. US20040010818A1 GENERAL INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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Pred. No. 1.8e-37;
; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/433,433
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
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US-10-734-947-1
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                                                                                            US-10-734-947-1
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                                Matches
                                              Query Match
Best Local :
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO O
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
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                                                                                                     NAME/KEY: misc feature
LOCATION: (6516)..(6516)
OTHER INFORMATION: n = A
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                              Score 154; DB 18; Pred. No. 1.8e-37; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                   Sequence 17, Application US/09906209; Patent No. US20020165385A1; GENERAL INFORMATION: APPLICANT: Allen, Steve; APPLICANT: Butler, Karla; APPLICANT: Carlson, Tom APPLICANT: Ilag, Lawrence L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6516)..(6516)
; OTHER INFORMATION: n = A,
US-10-734-947-1
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US-10-734-947-1/c
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US-09-906-209-17
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Publication No. US20040128714A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 154; Conserv
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TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
APPLICANT: Carlson, Tom
APPLICANT: Ilag, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: r
US-09-906-209-17
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APPLICANT: Ilag, Lawrence L.
TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
FILE REFERENCE: BB1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SOPTWARE: Microsoft Office 97
SEQ ID NO 17
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; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n
US-09-906-209-17
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; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
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US-09-934-900-26
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Best Local Similarity 100.0%; Pred. No. 9.8e-
Matches 112; Conservative 0; Mismatches
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Matches
GENERAL INFORMATION:
               Sequence 26, Appropriate Publication No.
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APPLICANT: Butler
APPLICANT: Carlso
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TYPE: DNA
ORGANISM: synthetic
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             Application US/09934900 vo. US20030054521A1
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APPLICANT:

Cahoon, Rebecca Hitz, William D

APPLICANT: Booth,

Russ

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TITLE OF INVENTION: Nucleotide Sequences of TITLE OF INVENTION: ACP Desaturase FILE REFERENCE: BB1476 US NA CURRENT APPLICATION NUMBER: US/09/934,900 CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/226996 PRIOR FILING DATE: 2000-08-22 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Microsoft Office 97 SEQ ID NO 26 LENGTH: 6611
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; TITLE OF INVENTION: Nucleotide Sequences of a ;
TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/22696
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
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Best Local :
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                                                                                                                                                                                          FEATURE:
NAME/KEY: Unsure
LOCATION: (4436)..(4436)
OTHER INFORMATION: n = A
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NAME/KEY: Unsure
LOCATION: (4436)..(4436)
OTHER INFORMATION: n = A, C,
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LENGTH: 6611
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Local Similarity 97.7%;
                                                                                                                                      Local Similarity
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                                                            ATGAGCGAGATGACCAGCTCCGGCCG 154
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Yadav, Naren
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Hitz, William D
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llarity 97.7%;
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                                                                                                                                  Score 82.8; DB:
Pred. No. 7e-16;
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RESULT 19
US-10-981-293-26
; Sequence 26, App
; Publication No.
                                TITLE OF INVENTION: Nucleotide Sequences of a New Class of TITLE OF INVENTION: ACP Desaturase FILE REFERENCE: BB1476 US NA CURRENT APPLICATION NUMBER: US/10/981,293 CURRENT FILING DATE: 2004-11-04 PRIOR APPLICATION NUMBER: US/09/934,900 PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/22696 PRIOR FILING DATE: 2000-08-22 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Microsoft Office 97
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APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren

TITLE OF INVENTION: Nucleotide Sequences of a New Class of
TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR APPLICATION NUMBER: 60/22696
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
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SEQ ID NO 26
LENGTH: 6611
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APPLICANT: Cahoon, Re
APPLICANT: Hitz, Will
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LOCATION: (4436)..(4436)
OTHER INFORMATION: n = A
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Hitz, William
                                                                                                                                                                                                                                               Kinney, Anthony
Yadav, Naren
                                                                                                                                                                                                                                                                                    Cahoon, Rebeco
Hitz, William
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No. US20050066390A1
                                                                                                                                                                                                                                                                                                                                                                              Application US/10981293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.8%;
nilarity 97.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                              US20050066390A1
                                                                                                                                                                                                                                                                                    Rebecca
William D
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Villiam D
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                                                                                                                                                                                                                            Diverged Delta-9 Stearoyl-
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APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND FILE REFERENCE: BB1449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO 29

LENGTH: 963

TYPE: DNA
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                                                                                                                                                                                                                                     RESULT 22
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US-09-887-194A-29
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                         APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 97.7
84; Conservative
                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Glassman, Kimberly F.
                                                                                                                                                                                         Sequence 29, Application US/09887194A Publication No. US20030036197A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Applica Publication No. US20 GENERAL INFORMATION:
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Best Local
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                NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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81; Conservative
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Lowe, Keith S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09887194A
No. US20030036197A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nichols,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lassman, Kimberly F. Gordon-Kamm, William
Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
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Pred. No.
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Pred. No. 7e-16;
); Mismatches
                                                                                                                                                                                                                                                                                                             154
                                                                                                                                                                                                                                                                                 963
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2.7e-15;
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                                                                        EXPRESSION
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RESULT 24
US-09-887-194A-12/c
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                                                                                                                                                                                                    Sequence 12, Application US/09887194A Publication No. US20030036197A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09887194A
Publication No. US20030036197A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Office SEQ ID NO 12
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Best Local
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                                                                                          APPLICANT:
                                                                                                                                               APPLICANT: Glassman, APPLICANT: Gordon-K
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TYPE: DNA
ORGANISM: Artificial S
FEATURE:
      TITLE OF
                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/887,194A CURRENT FILING DATE: 2002-03-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Glassman,
                                       APPLICANT
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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        INVENTION:
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Gorus Kinney, And Lowe, Keith S.
Lowe, Keith S.
Nichols, Scott E.
The Company of 
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Yowe, Keith S.
                                                                                                                                                                                                                                                                                                                                                                                                        GAGATGACCAGCTCCGGCCG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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      RECOMBINANT CONSTRUCTS AND THEIR USE
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                                                                                                                                               Kimberly F. amm, William
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k; Pred. No. 6.3
0; Mismatches
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Pred. No.
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2.7e-15;
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        N REDUCING GENE EXPRESSION
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RESULT 26
US-09-934-900-24/c
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
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US-09-934-900-24
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
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Best Local Similarity 100.
Matches 80; Conservative
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LENGTH: 80
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CURRENT APPLICATION NUMBER: US/0:
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
EQ ID NO 24
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/9: CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/226996 PRIOR FILING DATE: 2000-08-22 NUMBER OF TO NO. 26
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APPLICANT: Cahoo
APPLICANT: Hitz,
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Yadav, Naren
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Hitz, William D
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100.0%; Pred. No. 6.3e-15;
tive 0; Mismatches 0;
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CTCGACGATGAGC 60

CGACGATGAGC 97

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TITLE OF INVENTION: Nucleotide Sequences of TITLE OF INVENTION: ACP Desaturase FILE REFERENCE: BB1476 US NA CURRENT APPLICATION NUMBER: US/10/981,293 CURRENT FILING DATE: 2004-11-04 PRIOR APPLICATION NUMBER: US/09/934,900 PRIOR FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/226996 PRIOR APPLICATION NUMBER: 60/226996 PRIOR FILING DATE: 2000-08-22 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Microsoft Office 97 SEQ ID NO 24 LENGTH: 80 TYPE: DNA
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APPLICANT: Yadav, Naren
IITLE OF INVENTION: Nucleotide Sequences of
IITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 80
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Best Local S
Matches 80
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Best Local Similarity
Matches 80; Conser
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Publication No.
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APPLICANT:
APPLICANT:
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                                                                                    ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: region of pKS106 and pKS124
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Yadav, Naren
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Hitz, William
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Hitz, William D
51.9%; Score 80; DB 19; llarity 100.0%; Pred. No. 6.3e-15; Conservative 0; Mismatches 0;
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William D
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6.3e-15;
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RESULT 29
US-09-887-194A-14
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US-10-981-293-24/c
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                                                                                   APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND TH
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                      Publication No.
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Best Local Similarity 100
Matches 80; Conservative
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SEQ ID NO 24
LENGTH: 80
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                                                     LENGTH: 92
TYPE: DNA
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                              ORGANISM: Artificial Sequence
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  OTHER INFORMATION: Description
                     FEATURE:
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Lowe, Keith S.
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vo. US20030036197A1
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Yadav, Naren
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Hitz, William
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No. US20050066390A1
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LENGTH: 92

TYPE: DNA

CORGANISM

COURAGE: Microsoft Office 97

SEQ ID NO 14

LENGTH: 92

TYPE: DNA

CORGANISM

COMMINANT

LENGTH: 92

TYPE: DNA

CORGANISM

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CONSTRUCTS AND

LENGTH: 92

TYPE: DNA

COMMINANT

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US-09-887-194A-24
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US-09-887-194A-14/c
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                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                        APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
                                                                                                                                                                                                                                                                                                     APPLICANT: Glassman, Kimberly F.
APPLICANT: Gordon-Kamm, William
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
                                                                                                                                                         NUMBER OF SEQ
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.9%; Score 80; DB 10; llarity 100.0%; Pred. No. 6.2e-15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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6.2e-15;
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                                                                        APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
ITITLE OF INVENTION: QUORUM SENSING SIGNALING IN
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-389-647-277
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APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AN
FILE REFERENCE: BB1449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
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SEQ ID NO 24
LENGTH: 1717
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                   Sequence 277, Application US/10389647 Publication No. US20040033549A1 GENERAL INFORMATION:
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Publication No. US20030036197A1
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   ORGANISM: Pseudomonas aeruginosa
-10-389-647-277
                              EQ ID NO 277
LENGTH: 1251
TYPE: DNA
                                                                                                                                                                                                                                                                  APPLICANT: GREENBERG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Glassman, Kimberly F.
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: region of pBS68
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Thee, Keith S.
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95.9%;
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Pred. No. 0.00
0; Mismatches
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Pred. No. 0.00013;
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NUMBER OF
SEQ ID NO
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RESULT 35
US-10-156-761-6327
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-277
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US-10-389-647-277/c
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TITLE OF INVENTION: QUORUM SENSING SIGNALING IN
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 1999-09-03
                                 APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
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                                                                                                                                                                                                                                                                                                                    Sequence 6327, Application US/10156761 Publication No. US20030119018A1
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Best Local Similarity
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APPLICANT: SCHUSTER,
APPLICANT: LOSTROH, (
PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC
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HORIKAWA, HIROSHI
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nilarity 61.6%;
Conservative (
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RESULT 37
US-10-156-761-1
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; LOCATION: (1)..(1581)
US-10-156-761-6327
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US-10-156-761-6327/c
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; LOCATION: (1)..(1581)
US-10-156-761-6327
                                                 GENERAL INFORMATION:
APPLICANT: OMURA, SA
APPLICANT: IKEDA, H
APPLICANT: ISHIKAWA
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                                                                                                                Sequence 1, Application US/10156761 Publication No. US20030119018A1
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Best Local Similarity
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SEQ ID NO 6327
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Streptomyces
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces
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IKEDA, HAKULISHIKAWA, JUN
ISHIKAWA, HIROSHI
HORIKAWA, HIROSHI
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HORIKAWA, HIROSHI
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59.1%;
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Pred. No. 0.029;
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; LOCATION: (4187715)
; OTHER INFORMATION: a, t
US-10-156-761-1
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; LOCATION: (4187715)
; OTHER INFORMATION: a, t
US-10-156-761-1
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 9025608
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SEQ ID NO 1
LENGTH: 9025608
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Best Local Similarity
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APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                FEATURE:
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 7618860
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 CCCGAGCAGTTCGCCGGGCTCGTCCGGGCGTCGCAGTACGGAGGCGA
                         CCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCCGGCCCGGAGCTGG
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ilarity 59.1%;
Conservative
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Pred. No.
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ced. No. 0.018;
Mismatches 45;
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0.018;
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                                                                                             Length 9025608;
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                         rcarcrectear 63
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CGACCTCGCGGTT 7618801
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RESULT 40
US-10-437-963-43250/c
; Sequence 43250, Application US/10437963
; Publication No. US20040123343A1
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US-10-437-963-43250
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 43250
LENGTH: 1821
                       APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 43250
LENGTH: 1821
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Best Local (
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APPLICANT:
APPLICANT:
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OTHER INFORMATION: Clone
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: Kovalic, David I
: Zhou, Yihua
: Cao, Yongwei
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Wu, Wei
Boukharov, Andrey F
Barbazuk, Brad
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Kovalic, David )
Zhou, Yihua
Cao, Yongwei
Oryza sativa
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                                                                                                                                                                                 Boukharov, Andrey A.
Barbazuk, Brad
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RESULT 42
US-10-437-963-51952/c
; Sequence 51952, Application US/10437963
; Publication No. US20040123343A1
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_54296C.1
US-10-437-963-51952
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US-10-437-963-51952
; Sequence 51952, Application US/10437963
; Publication No. US20040123343A1
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 51952
LENGTH: 742
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Best Local Similarity
Matches 79; Conserv
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                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.2
les 64; Conservative
                                                                          INFORMATION:
ANT: La Rosa, Thomas
ANT: Kovalic, David
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Cao, Yongwei
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Kovalic, David
Zhou, Yihua
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                                Cao, You
Wu, Wei
Boukharov, And
Barbazuk, Brad
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Barbazuk, Brad
Li, Ping
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Pred. No. 0.058;
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RESULT 44
US-10-437-963-85043/c
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone
US-10-437-963-85043
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US-10-437-963-85043
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Best Local S
Matches 64
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 85043
LENGTH: 561
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 51952
LENGTH: 742
TYPE: DNA
ORGANISM: Oryza sativa
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APPLICANT:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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OTHER INFORMATION:
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Cao, Yongwei
                                                                                                 ATGACCAGCTCC 149
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Barbazuk, Brad
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Mole;
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 85043
LENGTH: 561
TYPE: DN"
                                                               ; FEATURE:
; OTHER INFORMATION:
US-10-437-963-36912
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US-10-437-963-36912
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                                                                                                                                            SEQ ID NO 36912
LENGTH: 816
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Matches
    Best Local Similarity Matches 69; Conserv
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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ORGANISM: Oryza sativa
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Cao,
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Li. pin-
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                                                                             Clone ID: PAT_MRT4530_40691C.1
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Score 36; DB 18 Pred. No. 0.12; 0; Mismatches
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Search Job tin	DЪ	VΩ	Дb	δō	DЬ	Ş
Search completed: April 9, 2005, 01:03:46 Job time : 528 secs	538 GCCG 541	151 GCCG 154	478 CACCACCACCACCAGACGCCGCCGCCGCCGCCACTCCGGCACTACTCAGCCCC 537	91 GATGAGCGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCG 150	418 GAGCGCGAGCACGGATCCGGCCGCCGCCGCCACCATGACCTCGTCGGCCGCCGCCGCCGCCGCAC 477	31 GAGTCGGCGGCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGGC

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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous
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Pred. No. 2.7e-28;
Mismatches 0;
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y repeat region DNA
the invention
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RESULT 3
AAD32908
ID AAD3
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AC AAD3
XX O1-J
XX O1-J
XX Plas
XX Rice
KW Rice
KW Rice
KW Gil,
KW Rice
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Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the sequences and their reverse genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is 2% ELVISLIVES complementary repeat region DN found in plasmid pKS133 used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD32908 standard; DNA; 154
 22-AUG-2000; 2000US-0226996P
                                                                                       WO200216565-A2
                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-2002
                              22-AUG-2001; 2001WO-US026246
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                                                                                                                                                                                                                                                                                                                                                                    transgenic
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Similarity 100.0%;
54; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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complement(82. .111)
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                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                  fatty acid desaturase;
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Pred. No. 2.7e-28;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                 saturase; enzyme; cellular lipid;
immunisation; plasmid pKS133; ge
                                                                                                                 protein
                                                                                                                                                          protein"
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음 성 음

61

CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCA

120

60

154 154 CATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120

음 중

121 121

ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG

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                                                                                                 The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in the larges or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce is IX ELVISLIVES complementary repeat region DNA found in plasmid pXS133 cc suppression of Fad2 in soybean
                                              Query Match
Best Local (
                                  Matches
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                                                                                               Sequence
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                                                 Similarity
   CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGAGCTGGTCATCTCGCT
                                                                                              154 BP; 24 A;
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                                  Conservative
                                              100.0%;
                                                                                               53 C;
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                              ; Score 154; DB 6; I; Pred. No. 2.7e-28;
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                                Indels
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                                  0,
                               Gaps
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RESULT 4
AAD32908/c
ID AAD32908;
XX
AC AAD32908;
XX
DT 01-JUL-200
XX
DE Plasmid pl
XX
CW Rice; div
KW Rice; div
KW oil; tran
KW oil; tran
KW ds.
XX
CS Unidentif
XX
FH Key
FT CDS
FT CDS
FT CDS Plasmid pKS133 2X ELVISLIVES complementary repeat Unidentified 01-JUL-2002 transgenic diverged standard; DNA; 154 (first entry) delta-9 c plant; /product= /*tag= Location/Qualifiers .36 gene fatty acid desaturase; рJ "ELVISLIVES mapping; protein" enzyme; DNA. ce llular lipid; id pKS133; gene;

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RESULT 5
ADQ07968
ID ADQ0
XX
AC ADQ0
XX
DT 23-S
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Matches 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, poly and unsaturated fatty acids and in increasing the unsaturation levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-2000; 2000US-0226996P
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 23-SEP-2004
                                                       ADQ07968
                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and unsaturated fin cellular lipids.
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                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                               100.0%; Score 154; DB 6; ilarity 100.0%; Pred. No. 2.7e-28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        BP;
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 (first
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complement(82. .111)
/*tag= c
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                                                        DNA;
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  entry)
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dairy product; pet food product; animal feed; ss
                                                                                                                                                                                                                                                                                                                                            pKS151; seed specific promoter; gene silencing; chalcone transgenic; liquiritigenin-derived isoflavone; isoflavone food product; snack food product; baked good product; frihealth food product; infant formula; beverage; nutritions
                                                                                                                                                                                                                                                                                                                                                                          Seed
                                                                                                                                                                                                                                                                                                         stem_loop
                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                  WPI; 2004-533136/51
                                                                                                                                                                                                                                                                11-DEC-2003; 2003US-00734947.
                                                                                                                                                                                                                                                     13-DEC-2002; 2002US-0433433P
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                                                                                                                                                                                                                                                                                                                                                                         specific
                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .154
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                                                                                                                                                                                                                                                                                                                                                                         silencing
                                                                                                                                                                                                                                                                                                                                                                          vector
                                                                                                                                                                                                                                                                                                                                                                         pKS151,
                                                                                                                                                                                                                                                                                                                                                                          stem
                                                                                                                                                                                                                                                                                                                                                                          loop
                                                                                                                                                                                                                                                                                                                                                   /onoid;
fried food product;
                                                                                                                                                                                                                                                                                                                                                                          gion.
                                                                                                                                                                                                                                                                                                                                              al supplement;
                                                                                                                                                                                                                                                                                                                                                              reductase;
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Decreasing ratio of liquiritigenin-derived isoflavones isoflavones in a plant comprises transforming plant cel acid sequence showing homology to sequence encoding cha (deoxychalcone synthase). nes relative to total cell with nucleic chalcone reductase elative to total with nucleic

Example 7; SEQ ID NO 7; 25pp; English

The invention relates to decreasing the ratio of liquiritigenin-derived construct comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct parts of the plant, an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product to the total isoflavone levels obtained from the seeds or plant parts, a condict of liquiritigenin-derived isoflavones relative to incorporated the isoflavonoid-containing product, and a method of corporated the isoflavonoid-containing product, and a method of liquiritigenin-derived isoflavones relative to the total isoflavone forms a loop in the stem-loop structure. The nucleic acid sequence forms a loop in the stem-loop structure and the stem comprises a sequence of ADQ07969. The promoter is a seed-specific producing an isoflavone relative to the total isoflavones in an isoflavone-containing product which has seed-specific producing plant. The methods and recombinant construct are useful in creal food product, snack food product, baked good product, fried food product, snack food product, baked good product. The present construct is interested in fired and the single ment, dairy product, pet food product, or animal feed. The present construct is the single stranded version of the stem loop region from the present sequence is the single stranded version of the stem loop region from the present sequence. plasmid pKS151.

Sequence 154 B₽; 24 A; 53 ç, 53 ç, 24 .. 0 **;** 0 Other;

밁 Ş Query Match Best Local S Matches 154 100.0%; il Similarity 100.0%; 154; Conservative 0 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60 0 Score 154; DB 12; Pred. No. 2.7e-28; Mismatches 0; Length TEGTCATCTCGCT 60 154; Gaps 0

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RESULT 6
ADQ07968/c
ID ADQ079
XX ADQ079
XX ADQ079
XX ADQ079
XX ADQ079
XX ADQ079
XX PROPERTY Seed B
XX PROPERTY SEEM_1
FT SEEM_1
CC The incorp
CC Constract
CC Constract
CC Constract
CC Constract
CC Constract
CC FROOD
XX MCGON
XX PPI DECREA
PT SEEM_1
CC FOOD
CC The incorp
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CC SEQUET
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CC SEQUET
CC Livelic
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CC Grooduc
CC Produc
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The invention relates to decreasing the ratio of liquiritigenin-derived construct comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct to a plant parts of the plant, an isoflavone reductase cDNA). Also included acre an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product to the total isoflavone levels obtained from the seeds or plant parts, a concorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product, and a method of converse a loop in the stem-loop structure. The nucleic acid sequence forms a loop in the stem-loop structure. The stem comprises a sequence of ADQ07968). The promoter is a seed-specific producing plant. The method is useful for decreasing the ratio of liquiritigenin derived isoflavones relative to the total isoflavone-specific producing plant. The methods and recombinant construct are useful in producing an isoflavonoid-containing product which is incorporated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic; li
food product;
health food pro
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RESULT 7
ADF89887
ID ADF8
XX
ADF89887
AC ADF8
XX
AC ADF8
XX
CAPT
CAPT
CAPT
CAPT
CAPT
ADF89887
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Best Local S
Matches 154
The invention relates to a plant comprising at least one recombinant DNA molecule comprising a promoter operably linked to at least a portion of at least one oxidosqualene cyclase gene, the molecule sufficient to suppress the production of a triterpene or any of its progeny, where the progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultiflorenol or any combination. The plants are useful in generating products which may be used as feeds, foods, beverages and industrial products like agricultural adjuvants, concrete supplies, dielectric fluids, dust suppressants, fuel additives, hydraulic fluids, industrial cleaners, industrial lubricants, metalworking fluids, odor reduction, paint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidosqualene cyclase; triterpene; plant protectant; plant; soybean; beta-amyrin synthase; ds.
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beverages and
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cyclase to lower triterpene level, used as
industrial products like agricultural adju
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Pred. No. 2.7e-28;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         English.
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Saponins

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RESULT 8
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AC ADF898
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         The invention relates to a plant comprising at least one recombinant DNA molecule comprising a promoter operably linked to at least a portion of at least one oxidosqualene cyclase gene, the molecule sufficient to suppress the production of a triterpene or any of its progeny, where the progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultiflorenol or any combination. The plants are useful in generating products which may be used as feeds, foods, beverages and industrial products like agricultural adjuvants, concrete supplies, dielectric fluids, dust suppressants, fuel additives, hydraulic fluids, industrial cleaners, industrial lubricants, metalworking fluids, odor reduction, paint
                                                                                                                                                                                                                                                    beverages supplies.
                                                                                                                                                                                                                                                                 New transgenic plants comprising recombinant DNA molecules encoding oxidosqualene cyclase to lower triterpene level, used as feeds, foo beverages and industrial products like agricultural adjuvants or co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strippers, printing may play a defense regresents
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myrin synthase;
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RESULT 9
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Best Local S
Matches 154
                                       The invention relates to a method for increasing isoflavonoid production in a plant, by transforming the plant with a recombinant DNA construct having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone 3-hydroxylase, and second recombinant DNA construct having a PN encoding C1 myb and a R myc-type transcription factor, growing the transformed plant, and evaluating the quantity of isoflavonoid from the plant. The method of the invention is useful for increasing isoflavonoid production in an isoflavonoid-producing plant. The current sequence represents the seed-specific expression vector pKS151, into which a polynucleotide encoding a portion of soybean flavanone 3-hydroxylase was inserted in an example from the invention, for the transformation of Glycine max.
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Pred. No. 3.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flavanone
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Query Match Best Local Similarity

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Sequence

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                                                                                                                                                Query Match
Best Local S
Matches 154
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                                                                                                                                                                                                                                                                The invention relates to a method for increasing isoflavonoid production in a plant, by transforming the plant with a recombinant DNA construct having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone 3-hydroxylase, and second recombinant DNA construct having a PN encoding C1 myb and a R myc-type transcription factor, growing the transformed plant, and evaluating the quantity of isoflavonoid from the plant. The method of the invention is useful for increasing isoflavonoid production in an isoflavonoid-producing plant. The current sequence represents the seed-specific expression vector pKS151, into which a polynucleotide encoding a portion of soybean flavanone 3-hydroxylase was inserted in an example from the invention, for the transformation of Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing isoflavonoid production in an isoflavonoid-producing plant, comprises transforming a plant with recombinant DNA constructs, growing the transformed plant, and evaluating increased quantity of isoflavonoid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                   Similarity
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CATCGTCGAGTCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG
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                                                                                                                                                                                                                              2236 A;
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                                                                                                                                           Score 154; DB 12; Pred. No. 3.1e-28; Mismatches 0;
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                                                                                                                                                                                                                              2053 T;
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RESULT 11
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                                isoflavones relative to the total isoflavones in an isoflavonoid-
isoflavones relative to the total isoflavones in an isoflavonoid-
isoflavones relative to the total isoflavones in an isoflavonoid-
isoflavones relative to the total isoflavones in an isoflavonoid-
isoflavonoid-
isoflavonoid-promoter operably linked to a nucleic acid
sequence of at least 200 nucleotides having at least 75% sequence
identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
are an isoflavonoid-producing plant made by the method above, seeds or
plant parts of the plant, an isoflavonoid-containing protein product
having a reduced ratio of liquiritigenin-derived isoflavones relative to
the total isoflavone levels obtained from the seeds or plant parts, a
food (or a nutritional supplement, a food bar, or a beverage) which has
incorporated the isoflavonoid-containing product, and a method of
producing an isoflavonoid-containing product, and a reduced ratio of
liquiritigenin-derived isoflavones relative to the total isoflavone
                                                                                                                                                                                                                                                                                                                                                                                            Decreasing ratio of liquiritigenin-derived isoflavones isoflavones in a plant comprises transforming plant ce acid sequence showing homology to sequence encoding characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seed
                                                                                                                                                                                                                                                                                                                                        Example 1;
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Cauliflower
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                                                                                                                                                                                                                                                                                                                                                                           (deoxychalcone synthase)
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B; ADQ07969.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli.
mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 supplement; dairy product; pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0433433P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003US-00734947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene silencing vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 5457. .5486
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/note= "No start or stop codon
/product= "ELVISLIVES peptide"
                                                                                                                                                                                                                                                                                                                                      NO 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \boldsymbol{\omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus
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                                                                                                                                                                                                                                                                                                                                      25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຸໝ
                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pKS151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant; so
; baked go
nt formula;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product;
                                                                                                                                                                                                                                                                                                                                                                                               nes relative to toto cell with nucleic chalcone reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oybean;
ood product;
beverage;
 structure. The cture and the
                                                                                                                                                                                                                                                                                                                                                                                                                  elative to total with nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal feed; ds.
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RESULT 12
ADQ07962/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stem comprises a sequence of ADQ07968). The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin derived isoflavones relative to the total isoflavones in an isoflavone-producing plant. The methods and recombinant construct are useful in producing an isoflavonoid-containing product which is incorporated in cereal food product, snack food product, baked good product, fried food product, health food product, infant formula, beverage, nutritional supplement, dairy product, pet food product, or animal feed. The present sequence is the Seed specific gene silencing vector pKS151, into which the soybean cDNA is cloned (into the NotI site flanked by the stem regions of ADQ07968.
                                                                                                                                                                                                                                                                                                                                         isoflavonoid; food product; snack food product; fried food product; health food product; infant nutritional supplement; dairy product; pet food
                                                                                                                                                                                                                                                                                                                                                                                                                      Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                US2004128714-A1.
                                                                                                                                                                                                                                                                                          Escherichia coli.
Cauliflower mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ07962
WPI; 2004-533136/51.
P-PSDB; ADQ07969.
                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                    Glycine
                                                                                                                                                                                                                                                                                                                                                                                 transgenic;
                                                                                                                                                                                                                                                                                                                                                                                              pKS151; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-2004
                                    Mcgonigle
                                                                                       13-DEC-2002;
                                                                                                                11-DEC-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5571
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                                                                                                                                                                                                                                                                                                                    max.
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                                                              MCGONIGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                    Ø
                                                                                                                                                                                                                                                                                                                                          d specific promoter; gene silencing; chalcone reductase;
liquiritigenin-derived isoflavone; plant; soybean;
d; food product; snack food product; baked good product;
product; health food product; infant formula; beverage;
supplement; dairy product; pet food product; animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                       2002US-0433433P
                                                                                                                2003US-00734947
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                      Location/Qualifiers
5457. .5486
/*tag= a
/partial
/note= "No start or stop codon sl
/product= "ELVISLIVES peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                    silencing vector pKS151.
                                                                                                                                                                                                                                                                                             virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Decreasing ratio of liquiritigenin-derived isoflavones isoflavones in a plant comprises transforming plant cel acid sequence showing homology to sequence encoding chalcone synthase).
                                                                                                                                                                           chalcone reductase
                                                                                                                                                                               elative to total with nucleic
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Example 1; SEQ ID NO 1; 25pp; English

cc producing plant comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct comprising a promoter operably linked to a nucleic acid construct of at least 200 nucleotides having at least 75% sequence care an isoflavonoid-producing plant made by the method above, seeds or compared the plant, an isoflavonoid-containing protein product the total isoflavone levels obtained from the seeds or plant parts, a conditional supplement, a food bar, or a beverage) which has concurred incorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product, and a method of liquiritigenin-derived isoflavones relative to the total isoflavone containing product, and a method of producing an isoflavonoid-containing product, and a method of liquiritigenin-derived isoflavones relative to the total isoflavone containing product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone containing product having a reduced ratio of liquiritigenin comprises a stem-loop structure. The mucleic acid sequence of ADQ07968). The promoter is a seed-specific product, plant. The methods and recombinant construct are useful in product, pack food product, which is incorporated in corporated food product, peatone, infant formula, beverage, nutritional supplement, dairy product, pet food product, or animal feed. The present construe is the Seed specific gene silencing vector pKS151, into which construe to the NotI site flanked by the stem The isoflavones relative to the regions of ADQ07968. relates 6 decreasing the ratio of liquirit the total isoflavones in an isofl igenin-derived avonoid-

Sequence 7701 BP; 2236 Α; 1702 C; 1709 G. 2053 Ţ, 0 U; 1 Other;

밁 Š 밁 밁 S á Query Match Best Local S Matches 5544 5604 5484 154; 61 Similarity CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCA CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGC CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 100.0%; larity 100.0%; Conservative <u>,</u> Score 154; DB 12; Pred. No. 3.1e-28; Mismatches 0; 5451 154 Length Indels 7701; GGTCATCTCGCT CICCGGCCGCCG <u>.</u> Gaps 120 5485 5545 60 0

ABK10072 standard; DNA; 4974

RESULT 13
ABK10072
ID ABK10
XX
AC ABK10
XX
DT 05-JU
XX
Plasm
XX
Plasm
XX
Plast
XX
PN EP117
XX
PD 23-JJ
XX ABK10072;

Plastidic phosphoglucomutase; gene; ₫ø; plasmid

Plasmid pKS133

DNA.

05-JUN-2002

(first

Synthetic EP1174510-A2

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RESULT 14
ABK10072/c
ID ABK10
XX
AC ABK10
DT 05-JU
XX
Plasm
XX
Plasm
XX
Plast
XX
Plast
XX
PN EP117
XX
PD 23-JA
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to plastidic phosphoglucomutase polypeptides and contrarsgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Contrarsgenic plant from the transformed plant cell. Contrarsgenic plant are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the contrar cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the polynucleotide, and comparing the level of the polypeptide in the polypeptide in the polypeptide in the polypeptide in the level of the polypeptide in a plant cell containing the isolated polynucleotide with the contaited polynucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed containing the level of the polypeptide in a plant cell that does not contain the containing the level of expression of the polynucleotide. A method for altering the level of expression of the polynucleotide in a plant cell that does not contain the containing the level of expression of the polynucleotide in the polynucleotide in a host cell comprises transformed contacted polynucleotide in the gene results in production of the chimeric gene, where the expression of the gene results in production of altered contain the methods of the invention. Note: This sequence is not confident in the printed specification but is based on sequence in a formation supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 112
                                                                                                                                                                                                                               )072/c
ABK10072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2000; 2000US-0218712P
                                              EP1174510-A2
                                                                                                                                      Plasmid pKS133 DNA
                                                                                                                                                                      05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-156692/21.
                                                                                                         Plastidic
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112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4974
                                                                                                                                                                                                                                standard; DNA; 4974
                                                                                                                                                                                                                                                                                                                                                                         CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
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                                                                                                         phosphoglucomutase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Butler KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 1444 A; 1070 C; 1003 G; 1456 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                72.7%; Sc
100.0%; P
itive 0;
                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                        gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                        ds;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5e-18;
hes 0;
                                                                                                        plasmid pKS133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Other;
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                                                                                                                                                                                                                                                                                                                                          112
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Best Local (
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                                                                                        Rice;
oil; t
                                                                                                                                       pBS68
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                terminator
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Location/Qualifiers 523. .725 /*tag= b

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transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. CC Polynucleotide fragments are useful for suppression the level of ce prosphoglucomutase activity. An isolated polynucleotide in a cc level of expression of a plastidic phosphoglucomutase polypeptide in a cc plant cell can be identified by introducing a DNA fragment comprising at cell containing the polynucleotide the level of the polypeptide in a plant cell containing the level of the polypeptide with cc the level of the polypeptide. A method for altering the level of expression of cell under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered contains of plastidic phosphoglucomutase. This sequence represents plasmid conformation supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated polypeptides having phosphoglucomutase ac polynucleotides encoding the polypeptides, useful for protransgenic plants with altered plastidic phosphoglucomutations.
Unidentified
                                                                                                                                          01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-2001;
                                                                                                                                                                                                                       AAD32909 standard; DNA; 6611
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                                       transgenic
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                                                                                                 plasmid used for diverged delta-9 desaturase suppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
112; Conserv
                                                           diverged delta-9 fatty acid desaturase;
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                                                                                                                                                                                                                                                                                                                                                                                                         GACCAGCTCCGGCCGCCGACTGACGATGAGCGAGATGACCAGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0
                                                                                                                                                                                                                                                                                                                              GACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.7%;
ilarity 100.0%;
Conservative
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                                       plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lates to plastidic phosphoglucomutase cleic acids. The sequences are useful by transforming a plant cell with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO 17;
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                                                                                                                                         entry)
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                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 112; DB 6;
Pred. No. 4.5e-18
); Mismatches (
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                                        enzyme; ce
ion; plasm
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                                        llular lipid;
id pBS68; ds.
                                                                                                                                                                                                                                                                                                                              GGCCG 4863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974;
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                                                                                                    ession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tivity and
                                                                                                                                                                                                                                                                                                                                                                   GCCG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other;
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RESULT 16
AAD32909/c
ID AAD32909;
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AC AAD32909;
XX
DT 01-JUL-200
XX
DE pBS68 plas
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                                                                                                                                                                                                                                                                                                                                  The present invention relates to diverged delta-9 fatty acid desaturase proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular lipids, including oil, in tissues when the enzyme is absent or rate-climiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce antibodies specific for the peptides and proteins. The present sequence is plasmid pBS68 which is used for the suppression of diverged delta-9 desaturase in high stearate phenotypes. This sequence is used in the expuence (AAD32909) corresponding to position 1501 to 6611 is not represented in the printed specification but is based on the sequence information supplied by the European patent office
                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                 Sequence
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- and unsaturated fatty acids and in increasing the unsaturation levels in cellular lipids.
                              01-JUL-2002
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 pBS68 plasmid used
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                                                                                                                                                            5408
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                            CATCGTCGAGTCGGCGGCCGCCGACT
                                                                                                                                                                                                                                                                                                                                  6611
                                                                                                                                                           CATCGTCGAGTCGGCGGCCGCTGAGT 5433
                                                                                                                                                                                                                                    CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT
                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cahoon
                                                                                                                                                                                                                                                                          53.8%; llarity 97.7%; Conservative
                             (first
                                                                                                                                                                                                                                                                                                                                 B₽;
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                                                                                                                                                                                                                                                                                                                                 1831 A;
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 for diverged delta-9 desaturase suppression.
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                             entry)
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                                                                                                                                                                                                                                                                                      Score 82.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                 C; 1453
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                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                      .4e-11;
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5373

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                                                                              Matches
                                                                                          Query Match
Best Local (
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oil; t
                                                                                                                              Sequence
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- and unsaturated fatty
in cellular lipids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Booth JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        delta-9 fatty acid desaturase polypeptides and polynucleotides, ful in creating transgenic plants having altered levels of mono-, polynusaturated fatty acids and in increasing the unsaturation levels
   129
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                                                                            84;
                                          AGTCGGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGC
                                                                                                                                6611 BP;
    ATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cahoon RE,
                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Hygromycin selection region"
3260. .5348
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Kit3
                                                                                                                               1831 A; 1472
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                                                                                        53.8%;
97.7%;
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Kit3_promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mapping;
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80. .1920)
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                                                                                           Score 82.8;
Pred. No. 5
                                                                                                                               C; 1453
                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinney
   154
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                                                                                           .4e-11;
                                                                                                                                1854 T;
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                                                                                                     Length
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                                                                              Indels
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                                                                                                                                -
                                                                                                       6611;
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id pBS68; ds.
                                                       GCCGACTCGACG
                                                                                                                                Other;
                                                                               <u>.</u>
                                                                              Gaps
                                                       128
                             5374
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RESULT 17
ABK10711
ID ABK10
XX ABK10
XX ARTII
XX Plast
XX
                                                                    The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of compression of a gene encoding a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at cell can be identified by introducing a DNA fragment comprising at plant cell containing the level of the polypeptide in the isolated polynucleotide with the level of the polypeptide in a plant cell that does not contain the cisolated polynucleotide. A method for altering the level of expression of the plastidic phosphoglucomutase protein in a host cell comprises call under conditions that are suitable for expression of the chimeric gene, where the expression of the gene results in production of altered contifical DNA used for plasmid construction, in the methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2001; 2001EP-00306143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polypeptides having phosphoglucomutase activity and polynucleotides encoding the polypeptides, useful for producing transgenic plants with altered plastidic phosphoglucomutase protein
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)B; AAU77109.
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/product=
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The invention relates to plastidic phosphoglucomutase polypeptides and their related nucleic acids. The sequences are useful for producing a transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the plant cell containing the polynucleotide, and comparing the level of the polypeptide in the pol
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from
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                                                                                                                                                                                                                                                                                                                                                                      New recombinant construct having a promoter operably linked to a sequence which when expressed produces an RNA having homology to mRNA and its reverse complement unrelated to endogenous DNA, for
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence when expressed by a host produces an RNA having homology to at leat target mRNA expressed by the host and complementary RNA regions. Trecombinant construct is useful for reducing the expression of a tmRNA or any similar endogenous mRNA. The RNAs expression of a tmRNA or any similar endogenous mRNA. The sequences and their rever complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic aci fragment which is in proximity to the DNA or RNA sequence derived it. The present sequence is 2X ELVISLIVES complementary region from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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DB; AAE18333.
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                                                                      expressed produces an complement unrelated
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                                                                        ked to a DNA ology to a target DNA, for reducing
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Claim

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Page 37;

77pp;

English

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RESULT 23
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XX O1-JU
XX O1-JU
XX Divex
KW Divex
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                  New delta-9 fatty acid desaturase polypeptides and polynucleotides, useful in creating transgenic plants having altered levels of mono-, and unsaturated fatty acids and in increasing the unsaturation levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diverged delta-9 fatty acid desaturase; enzyme; transgenic plant; gene mapping; immunisation; plasmid pKS106; gene; ds.
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   in cellular
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P-PSDB; AAE20554.
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larity 100.0%;
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proteins and polynucleotides encoding such proteins. The nucleic acid sequences may be used to increase the level of unsaturation in cellular CC lipids, including oil, in tissues when the enzyme is absent or rate-CC limiting, to isolate cDNAs and genes encoding homologous proteins from the same or other plant species and to create transgenic plants in which the polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found, those cells. They are useful as probes for genetic and physical gene CC mapping and as markers, e.g. restriction fragment length polymorphism CC (RFLP) markers. The peptides can be used to immunise animals to produce is IX ELVISLIVES complementary repeat region DNA found in plasmids pKS106 and pKS124. This sequence is used in the exemplification of the invention for the suppression of Fad2 in soybean
RESULT 24
AAD32907/c
ID AAD32907;
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AC AAD32907;
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DT 01-JUL-200
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DE Plasmids plasmids plasmid pla
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   WPI; 2002-269353/31
P-PSDB; AAE20554.
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cc proteins and polynucleotides encoding such proteins. The nucleic acid desaturase groteins and polynucleotides encoding such proteins. The nucleic acid control of the same or character of the same or other plant species and genes encoding homologous proteins from the polypeptides are present at higher or lower levels than normal or in those cell types or developmental stages in which they are not normally found, thus altering the level of mono-, poly- and unsaturated fatty acids in those cells. They are useful as probes for genetic and physical gene mapping and as markers, e.g. restriction fragment length polymorphism (RFLP) markers. The peptides can be used to immunise animals to produce is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106 cor the suppression of Fad2 in soybean
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                     solated polypeptides having phosphoglucomutase activity and leotides encoding the polypeptides, useful for producing nic plants with altered plastidic phosphoglucomutase protein
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RESULT 26
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RESULT 27
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C artificial DNA used for plasmid construction, in the methods of the
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HI-BRED INT INC.
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New recombinant construct having a promoter operably linked to sequence which when expressed produces an RNA having homology tmRNA and its reverse complement unrelated to endogenous DNA, for gene expression.

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The present invention relates to a new recombinant construct comprises a promoter operably linked to a DNA when expressed by a host produces an RNA having homology target mRNA expressed by the host and complementary RNA recombinant construct is useful for reducing the express

truct. The sequence which y to at least one regions. The sion of a target

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RESULT 28
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ID AAD29232;
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Matches 80
                                                                                                                                                                                                                                                                                                                                                New recombinant construct having a promoter operably linked to a DNA sequence which when expressed produces an RNA having homology to a target mRNA and its reverse complement unrelated to endogenous DNA, for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expressed from the recombinant constructs are also used in reducing expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from it. The present sequence is a PCR primer used for amplifying ELVISLIVES complementary region DNA used in the exemplification of the invention
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The present invention relates to a new recombinant construct. The construct comprises a promoter operably linked to a DNA sequence which when expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target mRNA or any similar endogenous mRNA. The RNAs expression of a target mRNA or any similar endogenous mRNA. The sequences and their reverse complements can be used to reduce the expression of any endogenous genomic sequence that shares substantial similarity to nucleic acid fragment which is in proximity to the DNA or RNA sequence derived from
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                                                                                                                                                                                          New recombinant construct having a promoter operably linked to a sequence which when expressed produces an RNA having homology to mRNA and its reverse complement unrelated to endogenous DNA, for
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                                     The present invention relates to a new recombinant construct. The CC construct comprises a promoter operably linked to a DNA sequence which construct tomprises a promoter operably linked to a DNA sequence which combined the expressed by a host produces an RNA having homology to at least one target mRNA expressed by the host and complementary RNA regions. The recombinant construct is useful for reducing the expression of a target recombinant constructs are also used in reducing expression of a target complements can be used to reduce the sequences and their reverse complements can be used to reduce the expression of any endogenous complement which is in proximity to the DNA or RNA sequence derived from the present sequence is 2x ELVISLIVES complementary regions surrounding the the contains 2x ELVISLIVES complementary regions surrounding the the invention a soybean delta-9 desaturase gene used in the exemplification of the
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transgenic plant, by transforming a plant cell with a polymucleotide of the invention and regenerating a plant from the transformed plant cell. CC Polymucleotide fragments are useful for suppressing the level of expression of a gene encoding a polymetide having plastidic plant cell. CC phosphoglucomutase activity. An isolated polymucleotide in a CC plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polymeptide in a plant cell containing the polymucleotide, and comparing the level of the level of the polymeptide in a plant cell that does not contain the CC isolated polymucleotide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transformed CC gene, where the expression of the gene results in production of altered clevels of plastidic phosphoglucomutase. This sequence represents an artificial DNA used for plasmid construction. in the cartificial DNA used for plasmid construction.
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transgenic plant, by transforming a plant cell with a polypeptides and transgenic plant, by transforming a plant cell with a polynucleotide of the invention and regenerating a plant from the transformed plant cell. Polynucleotide fragments are useful for suppressing the level of expression of a gene encoding a polypeptide having plastidic phosphoglucomutase activity. An isolated polynucleotide that affects the level of expression of a plastidic phosphoglucomutase polypeptide in a plant cell can be identified by introducing a DNA fragment comprising at least 541 nucleotides, measuring the level of the polypeptide in the level of the polypeptide. A method for altering the level of expression of a plastidic phosphoglucomutase protein in a host cell comprises transforming a host cell with a chimeric gene and growing the transforming that are suitable.
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                                                                                                                     quorum sensing signalling in bacteria. The method comprises: providing a cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798), where the cell is responsive to a quorum sensing signal molecule such that a detectable signal is generated; contacting the cell with a quorum sensing signal molecule in the presence and absence of a test compound; and detecting a change in the detectable signal. The method and modulator identified by the method are useful for treating a biofilm-associated disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections, acne, periodontal disease, catheter-associated infections, and medical device-associated infections. Note: The sequence data for this patent was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ntifying a modulator of quorum sensing signaling in bacteria, useful treating a biofilm-associated disorder, comprises contacting the central advantage of a quorum sensing signal molecule in the presence and absence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a quorum sensing compound.
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                         Query Match
Best Local
                                                                                                                                                 cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798), where the cell is responsive to a quorum sensing signal molecule such that a detectable signal is generated; contacting the cell with a quorum sensing signal molecule in the presence and absence of a test compound; and detecting a change in the detectable signal. The method and modulator identified by the method are useful for treating a biofilm-associated disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections, acne, periodontal disease, catheter-associated infections, and medical device-associated infections. Note: The sequence data for this patent was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; Anti-HIV; Antimicrobial; Immunosuppressive; quorum sensing signalling; bacterium; quorum sensing combiofilm-associated disease; cystic fibrosis; AIDS; middacne; periodontal disease; gene; ds; PA4304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for identifying a modulator of quorum sensing signalling in bacteria. The method comprises: providing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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e ear infection;
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The invention relates to plant nucleotide sequences that direct seed-
cc leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
cc or constitutive transcription of an operatively linked nucleic acid
segment. The invention also relates to a method for augmenting a plant
cc genome and a method of identifying a gene, where its expression is
altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
cc canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
sorghum, rice or wheat. The polynucleotides and the polypeptides they
cencode are useful for manipulating crop plants to alter or improve
phenotypic characteristics, to produce large quantities of oil or
proteins, to incur resistance to insecticides, viruses or fungi, and to
incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
chave a high nutritional value with reduced apical dominance or dwarfism,
carly flowering or altered metabolic pathways. This sequence represents a
complete the invention. Note: The sequence data for this
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26-SEP-2001;
04-APR-2002;
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(MOUG/)
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(COOP/)
(CLAZ/)
(GLAZ/)
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(KATA/)
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GOFF S A.
KATAGIRI F.
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BRIGGS S P.
COOPER B.
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PROVART N.
RICKE D.
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PROVART N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2730;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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The invention relates to a nucleic acid probe for measuring human expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments,

g human gene leotide

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RESULT 38
ACH91679/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc encoding at least 8 amino acids of any of the 6888 amino acid sequences cfully defined in the specification. The probe is a single exon probe that chybridises under high stringency conditions to a nucleic acid molecule capressed in human cells or tissues. Also included are a spatially-capture seed in human cells or tissues. Also included are a spatially-capture seed in human cells or tissues. Also included are a spatially-capture seed in the plurality of single exon nucleic acid probes for measuring human comparising a plurality of grobes is separately captured expression, a vector comprising the single exon nucleic acid captured expression, a method of measuring human gene expression, a vector comprising the single exon contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an contiguous amino acids of any of the above-mentioned amino acid constitutions of selling and/or licensing single exon probes or microarrays to consider data that should be specifically to a peptide cited above, comethods of selling and/or licensing single exon probes or microarrays to consider the prosection and a computer-readable captured expression and a computer-readable captured expression and a plurality of records (each record including data on the expression, a method of providing captured exoression analysis. The probes may be used as tools for surveying captured exon, or in constructing genome-derived single exon microarrays. Comparession analysis. The probes may be used as tools for surveying captured exon, or in constructing genome-derived single exon microarrays. Comparession analysis, in priming the synthesis of nucleic acids, or in expressing the open acid of expressing and characterising gross single exon probe of the invention. Note: The sequence is a human captured to did not form part of the printed specification, but was obtained captured in electronic format directly from USPTO at the printed specification, but was obtained captured to the
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                              Human; probe; ss; gene expression; single exon probe; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                       Human genome
                                                                                                                                                                                                                                                                                                                                                             ACH91679
(PENN/)
(RANK/)
                                                                                                                                                             US2003194704-A1
                                                                                                                                                                                                                                                                                                                                                                                                  ACH91679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                    03-APR-2002;
                                                                                       03-APR-2002; 2002US-00029386
                                                                                                                         16-OCT-2003
                                                                                                                                                                                                                                                                                                                           29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
  PENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG 98
                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGCTGCGCGCCGCCGCCAGCCCAGGTGCTCGATGAGCAGCGGCGGCC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGACCAGCTCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCGGAGGCGAGTGCGGCGACCGCGCACCCAGCCGCAGCCAGAGGCGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
 a a
                                                                                                                                                                                                                                                                                    derived single exon probe #24874.
                                                    2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 111 A;
                                                                                                                                                                                                                                                                                                                           (first
 αg
                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 C;
                                                                                                                                                                                                                                                                                                                                                                                                  850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other;
                                                                                                                                                                                                                                                      ∄.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           850;
                                                                                                                                                                                                                                                     croarray;
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HANZEL

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RESULT 39
ADP24630
ID ADP2
XX
AC ADP2
XX
DT 18-N
XX
DE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid probe for measuring human gene compression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and conding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that the probability of the 6888 amino acid sequences (comprising at least 8 amino acid soft on the following the compression of the specification of the plurality of a nucleic acid molecule conditions to the acid probes of separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of providing the single exon microarray to contiguous amino acids of any of the above—mentioned amino acid sequences (optionally with conservative amino acid substitutions), and computer-readable or methods of selling and/or licensing single exon probes or microarrays to constitute the probes of any subscription, and a computer-readable of the storage medium which contains a database having a plurality of records cited above. The probes may be used as tools for surveying to each record including data on the expression of a single exon probe cited above. The probes may be used as tools for surveying their specific exon, or in constructing genome—derived single exon microarrays. Comparison the probes are used in identifying and characterising gross alternative splicing events in detecting and characterising gross alternative form probe of the invention. Note: The sequence is a human condition
                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                    18-NOV-2004
                                                                                                               ADP24630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                       489
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                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                             standard; cDNA;
                                                                                                                                                                                                    GCCTCTGCGTGGGCTGGGTGCGCGGTCGCCGCACTGGCCGCCTCCGGCC
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                                                                                                                                                                                                                                                                                                                                                           22.7%;
ilarity 56.5%;
Conservative
                                 (first entry)
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                                                                                                             1797
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                                                                                                                                                                                                                                                                                                                                                                                                                                    c;
                                                                                                                                                                                                                                                                                                                                                        Score 35; DB Pred. No. 19; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    362
                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 86
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H
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PRO polypeptide

encoding cDNA

SEQ

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ATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGC

TCCGGCC 711

ccecc 116

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                                                                     Query Match
Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteopaulic, mepatotropic, and respiratory. The PRO polypeptide, its antiasthmatic, hepatotropic, and respiratory. The PRO polypeptide, its of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as polypeptide is useful for treating an immune related disorder such as polypeptide is useful for treating an immune related disorder such as polypeptide is useful for treating an immune related disorder such as polypeptide is useful for treating an immune related disorder such as
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide encoded by ... antirneumacie, antiinflammatory, antiarthritic, antirneumacie, antipsoriatic of teopathic, antidiabetic, dermatological, antipsoriatic Arteopathic, antidiabetic, and respiratory activity. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treerythematosus, rheumatoid arthritis, diabetes mellitus, renal disease, or demyelinating diseases of the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark H,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2002; 2002US-0423394P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; gene; PRO; antiinflammatory; antiarthritic; antirheu immunosuppressive; osteopathic; antidiabetic; dermatolog antipsoriatic; antiallergic; antiasthmatic; hepatotropic gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-2003; 2003WO-US034312
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                                                                                                                                                                            invention
                                                                        65;
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                                                                                       Similarity
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                                                                 22.7%;
ilarity 56.5%;
Conservative
                                                                                                                                          ВР;
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                                                                                                                                          263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a novel isolated
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                                                                 Score 35; DB Pred. No. 20; 0; Mismatches
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                                                                                                                                        552
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20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eating e.g.
immune-mediated
or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nical;
                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pressive,
AGCAGGACCTGC
                                GTCATCTCGCTC
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                                                                 Gaps
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656
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RESULT 40
ADP24630/c
antiinflammatory, antidiabetic, dermatological, antipsoriatic, antiallergic, costeopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the college of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the college of the invention arthritis, a specifically binds to the plant of the property of the property of the control of the lung, and the control of the lung, and the control of the lung, the control of the lung of the 
                                                         eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyppneumonitis, a transplantation associated disease, graft present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated nucleic acid and the polypeptide encoded by it. A protein of the invention has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treating enerythematosus, rheumatoid arthritis, diabetes mellitus, immune-m renal disease, or demyelinating diseases of the central or perip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; osteopathic; antipsoriatic; antiallergic; an
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P-PSDB; ADP24631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2002; 2002US-0423394P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding cDNA
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ic; antidiabetic; dermatological
antiasthmatic; hepatotropic; re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antirheumatic;
                                                                                                   hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune-mediated
or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WI;
                                                              protein
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Query Match Best Local Similarity

22.7**%**; 56.5**%**;

Score Pred.

35; No.

DB 20;

Length 1797;

Sequence

263

P 645

Ç

552

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337

.. H 13;

0

U; 0

Other;

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RESULT 41
AAS18438
ID AAS18
XX AAS18
XX AAS18
XX I2-MP
XX Conti
XX Narbo
KW eryth
KW agric
XX Strep
XX US630
XX O5-NC
PP 05-NC
XX Nucle
PR 27-MP
XX Nucle
PR 27-MP
XX Nucle
PR 27-MP
XX Nucle
PR 1:
CC recom
CC repan
CC repan
CC repan
CC recom
CC Synth
CC recom
CC Synth
CC recom
CC Synth
CC recom
CC Synth
CC Recom
CC S. na
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                            Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                           The present invention relates to recombinant DNA vectors (cosmids) tencode for the narbonolide polyketide synthase (PKS) enzyme and vari narbomycin modification enzymes from Streptomyces narbonensis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycin, rapamycin, tylosin, narbomycin, picromycin, methylmycin and neomethymycin) for use in agriculture, medicine and health. The recombinant vectors may be used to produce polyketides in relatively yields. AAS18432-AAS18443 represent contig DNA sequences that encode S. narbonensis PKS enzymes
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                          narbonensis, useful
                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding narbonolide polyketide synthases narbonensis, useful for the recombinant production of pontable polyketide synthases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Narbonolide polyketide synthase; PKS; narbomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1998;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS18438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS18438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KOSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                M
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOSAN
                                                                                                                                                                  1681 BP;
                          CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
                                                                                                                                                                                                                                                                                                                                                  Col 18; 24pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGCTGCGCGCGCGCGCGCCAGGCCCAGGTGCTCGATGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATGACCAGCTCCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG 98
 CGCCGCAGGGCCGCCGACGGCACCGGCCAGGCGGAGAGGGGACCT
                                                       CTGGCGCCGCTGCTCAGCGGGCTCACCCGCGGGTCGCGGG
                                                                      CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCGGAGGCGGCGAGTGCGGCGACCGCAGCCGCAGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcdaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  narbonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rapamycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0107093P.
99US-00320878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00434288
                                                                                                                                                                 231 A; 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                         22.6%;
55.9%;
                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠
دي
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   narbonensis
                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                         Score
Pred.
                                                                                                                                                                  C; 580
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        picromycin;
                                                                                                                         34.8; 1
No. 22;
                                                                                                                                                                  G; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyketide
                                                                                                                                        BB
                                                                                                                                                                  T; 0
                                                                                                             52;
                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                  Ç
                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modification enzyme;
thylmycin; neomethymycin;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                  0 Oth
                                                                                                                                                                                                                                                                                                                                                                                           po
 egecegecege 541
                                                     CGCTCCGGTCGGC 483
                                                                                                                                       1681;
                                                                                                                                                                   er;
                                                                                                                                                                                                            n relatively high that encode for
                                                                                                                                                                                                                                                                                                                                                                                           lyketides, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                          from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Be.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caccaccc 597
                                                                                 REGICATOTOGOT 60
                                                                                                                                                                                                                                                                                                       yme and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAGGCGCAGG
                                                                                                                                                                                                                                                                                                                         (cosmids) that
                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652
                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 43
ADL91894
ID ADL91
XX
AC ADL91
XX
AC ADL91
XX
DT 20-MA
XX
DE Strep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 42
AAS18438/c
ID AAS18438
                                                                                                                                                                                                               Query Match
Best Local S
Matches 66
   Streptomyces
                           20-MAY-2004
                                                                     ADL91894
                                                ADL91894;
                                                                                                                                                                                                                                                                                      rapamycin, tylosin, narbomycin, picromycin, methylmycin neomethymycin) for use in agriculture, medicine and heal recombinant vectors may be used to produce polyketides i yields. AAS18432-AAS18443 represent contig DNA sequences
                                                                                                                                                                                                                                                                                                                                  The present invention relates to recombinant DNA vectors (cosmids) encode for the narbonolide polyketide synthase (PKS) enzyme and va narbomycin modification enzymes from Streptomyces narbonensis. The recombinant DNA vectors can be used to produce recombinant ketide synthases and a variety of different polyketides (e.g. erythromycinants).
                                                                                                                                                                                                                                                                                                                                                                                 The
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding narbonolide polyketide synthases from Streptomyces narbonensis, useful for the recombinant production of polyketides, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythromycin; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narbonolide polyketide synthase; PKS; narbomycin modification enzyme; erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethymycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KOSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6303767-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS18438;
                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                  narbonensis
                                                                                                                           481
                                                                                                                                                                      541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-065495/09.
                                                                                                                                                97
                                                                                                                                                                                         37
                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOSAN
                                                                                                                                                                éccécceccaeérecercececreseces
                                                                                                                                                                                    GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGACTCGACGATGAG
                                                                    standard; DNA;
                                                                                                                          cdaccedacceccecceccaccaccecec
                                                                                                                                     CGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG
                                                                                                                                                                                                                                                         1681 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                              Conservative
  narbonolide polyketide
                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcdaniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      narbonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                PKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0107093P.
99US-00320878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9908-00434288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding
                                                                                                                                                                                                                                                                                                                                                                                                    24pp;
                                                                                                                                                                                                                                                         231 A; 672 C;
                                                                                                                                                                                                                                                                                enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                         entry)
                                                                                                                                                                                                                        22.6%;
55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                    1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
ა
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    narbonensis
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                        Score 34.8;
Pred. No. 22;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                         580 G;
  synthase
                                                                                                                                                                                                                                                         198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyketide
                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                        Τ;
                                                                                                                                                                                                                                                                                       polyketides in relatively DNA sequences that encode
coding
                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                  6,
                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                       U; 0
                                                                                                                                                                                                                                Length 1681;
                                                                                                                                                                                                                                                                                                                                 (e.g. erythromycin,
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase
 sequence
                                                                                                                                                                                                                                                                                                           health.
                                                                                                                                                                                                                                                       Other;
                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                          Gaps
                                                                                                                                            154
                                                                                                                       424
                                                                                                                                                                                                                                                                                       high
for
                                                                                                                                                                 482
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                                                                                   Query Match
Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                          17-APR-2001;
18-MAY-2001;
18-MAY-2001;
                                                                                                                                                   The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represents a Streptomyces narbonensis narbonolide polyketide synthase coding
                                                                                                                                                a Streptomyces narbonensis sequence of the invention
                                                                                                                                                                                                                                      New isolated nucleic acid comprising a narbonolide polyke gene from Streptomyces narbonensis, useful for providing polyhydroxyalkanoate monomer for medical and industrial a
                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                   (SHER/)
(LIUH/)
(XUEY/)
                                                                                                                                                                                                                                                                                                     Sherman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces narbonensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   narbonolide polyketide synthase medical application; industrial
                                                                                                                                                                                                                                                                                                                          (ZHAO/)
                                           424
                                                                                                                                                                                                                                                                                2004-119267/12.
                                                                                                                                                                                                                     1;
                      61
                                                                                    66;
                                                                                                                                                                                                                                                                                                                        SHERMAN
LIU H.
XUE Y.
ZHAO L.
                                                                                              Similarity
                  CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
                                                       CGGCCGGAGCTGGTCATCTCGCTCATCGTCGGCGGCGGCGGCGGAGCTGGTCATCTCGCT 60
                                                                                                                           1681
CTGGCGCCGCTGCTCAGCGGGCTCACCCGCGGG
                                                                                                                                                                                                                     SEQ ID
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                        ; 2001US-00836821.
; 2001US-00860846.
; 2001US-00861289.
                                                                                                                                                                                                                                                                                                      Liu
                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-00271889
                                                                                                                                                                                                                    NO 7;
                                                                                                                                                                                                                                                                                                                                                        U
                                                                                                                                                                                                                                                                                                   H
                                                                                                                          231 A;
                                                                                                                                                                                                                                                                                                                                                        Ħ
                                                                                          22.6%;
55.9%;
                                                                                                                                                                                                                                                                                                     Xue
                                                                                                                                                                                                                  362pp;
                                                                                                                                                                                                                                                                                                 ۲,
                                                                                                                          672
                                                                                Score 34.8; D
Pred. No. 22;
0; Mismatches
                                                                                  0,
                                                                                                                          Ç
                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                     Zhao
                                                                                                                          580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; polyhydroxyalkanoa application; ds.
                                                                                                                          <u>ດ</u>
                                                                                                                          198
                                                                                                     DB
                                                                                                                          Ή,
                                                                                                    12;
                                                                                 52;
                                                                                                                          0
                                                                                                                          ď,
                                        écceacacacticcaridae 483
                                                                                 Indels
                                                                                                   Length
                                                                                                                          0
                                                                                                                        Other;
                                                                                                                                                                                                                                      applications.
                                                                                                    1681;
                                                                                                                                                                                                                                                         etide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te monomer;
                                                                                0; Gaps
                                                                                <u>,</u>
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RESULT 44
ADL91894/c
 15-OCT-2002;
              16-OCT-2003
                                                        narbonolide
medical appl
                                                                             Streptomyces
                                          Streptomyces
                                                                                                                        ADL91894
                            US2003194784-A1
                                                                                            20-MAY-2004
                                                                                                                              a
                                                       ide polyketide application; in
                                                                                                                       standard;
                                          narbonensis.
2002US-00271889
                                                                            narbonolide polyketide
                                                                                            (first
                                                                                                                      DNA;
                                                       industrial
                                                              synthase
                                                                                                                       1681
                                                      gene; polyhydroxyalkanoata application; ds.
                                                                            synthase
                                                                           coding
                                                                          seque
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e monomer;

nce #7.

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RESULT 45
AAS59803
ID AAS59
XX AAS59
AC AAS59
XX AAS59
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2001;
18-MAY-2001;
18-MAY-2001;
                                                                                                                21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represents a Streptomyces narbonensis narbonolide polyketide synthase coding sequence of the invention.
   Skeiky YAW,
L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS59803 standard; DNA; 1498
                                                                                                                                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                                                                          Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002
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SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in CC infections of bone, joints and the central nervous system, however it is constitutions of bone, joints and the central nervous system, however it is constitutions of bone, joints and the central nervous system, however it is constitutions of the inflammatory lesions associated with acne constitution and the presence or absence of P. acnes in a constitution and determining the amount of bound protein the proteins of the invention and determining the amount of bound protein the proteins of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as consymelinked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU67430-AAU67444 and AAU68011-AAU68015. Note: The sequence data for this patent did not form part of the printed conscription of the printed constitution of the printed conscription of
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  Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary
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Mismatches 0;
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stearoyl-acp desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
synthetic
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synthetic construct
other sequences; artificial sequences.
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Similarity 100.0%;
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/mol_type="unassigned I
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Pred. No. 1.1e-19;
Mismatches 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
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/note="ELVISLIVES complementary
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Patent: WO 0216565-A 26 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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llarity 97.7%;
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/mol_type="unassigned i
/db_xref="taxon:32630"
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/mol_type="unassigned DN/
/db_xref="taxon:32644"
/note="Plasmid pBS68"
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AX367144
Sequence
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Patent: WO 0216565-A 26 28-FEB-2002;
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larity 100.0%; Pred. No.
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larity 97.7%;
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 29
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region
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/db_xref="taxon:32644"
/note="Plasmid pBS68"
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Pred. No. 1.6e-06;
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Recombinant constructs and their use in Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (UINTERNATIONAL, INC. (US)
Location/Qualifiers
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Location/Qualifiers
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GAGATGACCAGCTCCGGCCG
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db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary
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Patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemours and Company
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary
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Sequence 24
AX392335
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Sequence 14 from Patent WO0200904.
AX367129
AX367129.1 GI:18855330
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Nucleotide sequences of a new class of
stearcyl-acp desaturase genes
patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemous
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GAGATGACCAGCTCCGGCCG 117
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                                        51.9%; Solarity 100.0%; I Conservative 0;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary
pXS124"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"
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RESULT 17
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/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"
                                                                                                                        /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Recombinant constructs and their use in reducing Patent: WO 0200904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US); PIONE INTERNATIONAL, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   2-deoxy-scyllo-inosose aminotransferase; 2-deoxy-synthase; carbamoyltransferase; dehydrogenase; gly ORF1; ORF2; ORF3; tacA gene; tacD gene; tbmA gene; gene; tbmD gene; tbmE gene; transport protein. Streptomyces tenebrarius Streptomyces tenebrarius Bacteria; Actinobacteria; Actinobacteria; Actinobacteria;
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synthetic construct
other sequences; artificial sequences
Sohng, J.K.
Direct Submission
Submitted (01-AUG-2003) Sohng J.K., Ch
100 Kalsanri, Tangjeongmyun, Asan si,
                                                                                                                  Kharel, M.K., Lee, H.C., Liou, K., Woo, J.S. and Sohng, J.K. An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarius
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Isolation and characterization of the tobramycin cluster from Streptomyces tenebrarius FEMS Microbiol. Lett. 230 (2), 185-190 (2004)
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tbmB gene; tbmC
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complement
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PPFDTPAMADAIEALLDDPELRERIAETAAPLPSAKYSLTTAADQLTDIYRELGVCV"
PPFTDTPAMADAIEALLDDPELRERIAETAAPLPSAKYSLTTAADQLTDIYRELGVCV"
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product="2-deoxy-scyllo-inosose synthase"
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TAELGF PIS PAYAPLHTNRLYAPASRRRFALGEEHEKRID PAR PHL PVCERLTRRLIT
FHHAALLGDESDMHDIAAAVAKVLRHHGELRA"
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2-deoxy-scyllo-inosose aminotransferase; 2-deoxy-scyllo-inosose synthase; carbamoyltransferase; dehydrogenase; glycosyltransferase; ORF1; ORF2; ORF3; tacA gene; tacD gene; tbmA gene; tbmB gene; tbmC gene; tbmD gene; tbmB gene; transport protein.
Streptomyces tenebrarius
Streptomyces tenebrarius
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                  xnare1,M.K., Lee,H.C., Liou,K., Woo,J.S. and Sohng,J.K. An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarina
                                                                                                                                                                                                                                                                                                                                                                                      Isolation and characterize cluster from Streptomyces FEMS Microbiol. Lett. 230
                                                                                                                                                                               Unpublished
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/codr"
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58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                          tenebrarius (2), 185-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee,H.C.,
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                                                      Chemistry,
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                                                    Sun
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                                                    University,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="tbmB"
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|strain="ATCC 17920"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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    AVGVSFGLVQWALVLADTRLQDAITGPARATVTSVVGFGSEVASVGFYLAAGAVSTVT
SMSTLVAWFAVPLVLIAVVAFRWLRREPCPTGQVRPEPEPRRRD"
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/note="ORF2"
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/gene="tbmE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/db_xref="GI:45544457"
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RGVWHGFSYPVVPGHEWSGTVVEVNGPGAELVGRDVVGDLTCACGSCAACGRGTPVLC
ENLQELGFTRDGACAEYMTIPTGNLHVLPEGLSLRAACQVEPVAVALHAVSTVGVEPG
ERVAVLGAGGIGLMLMQVARQRGGVITTVGEPVARERRAVAAQLGARTVTTGRPGELAE
LVAKHPDLTPDVVLEASGYPVAVQEAIEVVRPGGRIGLVGYRVEEVGPMATHHVAVKA
LTIRGSLGPGGRFPEAIDLLARGEIEVEPLLSHEFALDDHARALDLALRRAEGNVRSF
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/gene="tacD"
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O; Mismatches
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2759 60 1; CDS

CDS gene

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BX571966_27
BX571966_28
BX571966_29
BX571966_30
BX571966_31
Continuation (9 of
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Best Local Similarity
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                                   ACGGGCGTCGCCTCGCGAGCTGTACGAGCTGCGCGATCGGCTCGGCC
                                                                    ACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGC
                                                                                                                                     GAGCTGGTCATCTCGTCATCGTCGAGTCGGCCGCCGACTCGACGATGAGCGAGATG
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Pred. No. 2.2e+02;
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                                                                                                                                                      'Protein name confidence' is used to rate our confidence accuracy of the protein name.

Class 1: Function experimentally demonstrated in P. a Class 2: Function of highly similar gene experimental demonstrated in another organism (and gene cont in terms of pathways its involved in, if known)

Class 3: Function proposed based on presence of conse acid motif, structural feature or limited seque to an experimentally studied gene.

Class 4: Homologs of previously reported seque or no similarity to any previously reported sequenations.
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2 (bases 1 to 10348)
Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Seattle, WA 98195, USA
3 (bases 1 to 10348)
                                                                                                                                                                                                                                                                                                                                                                           This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-FEB-2003) Department of Molecular Bi Biochemistry, Simon Fraser University, 8888 Univer Burnaby, British Columbia V5A 186, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406
20437337
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Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
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Pseudomonas aeruginosa PAO1
Bacteria; Proteobacteria; Gammaproteobacteria;
Pseudomonadaceae; Pseudomonas.
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)2...919
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)2. .919
                                                                                                  organism="Pseudomonas
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SGDTRFNVKADGSDLVQSRRLPESGFLASTLKTSINVNPVVLGLCLPLLCGSTALTDL
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COMplement (2640. . 2924)
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complement (5483...6748)
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based on presence of conserved amino acid restructural feature or limited sequence sime experimentally studied gene)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMLVGLTGNRLPEQTLRLMICAALDVVVQITRLASGRRC
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/locus_tag="PA4301"
complement (4602. .5486)
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LGLQLLGCYALWRMLKSV"
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                                                                                                                                          gene
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AE004846.
AE004846.
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Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington Genome Center, University Of Washington, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warre Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spence Wong, G.K.-S., Wu, Z. and Paulsen, I.T.

Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

Nature 406 (6799), 959-964 (2000)
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Pseudomonas aeruginosa PAO1
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 10348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa Community Annotation Project (PseudoCAP) Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Protein name confidence' is used to race our construction accuracy of the protein name.

Class 1: Function experimentally demonstrated in P. aeruginosa.

Class 2: Function of highly similar gene experimentally
demonstrated in another organism (and gene context consistent
in terms of pathways its involved in, if known).

Class 3: Function proposed based on presence of conserved amino
acid motif, structural feature or limited sequence similarity
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                                                                                                                                                                                                                                                                                                                                                                                        to an experimentally studied gene.
4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.
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.1 GI:9950517
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                     locus
                                                                                                                                                                    db_xref="taxon:208964"
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                                                                                                                                                                                                                                                                       organism="Pseudomonas aeruginosa PAO1"
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aeruginosa PAO1
                                                                                                                   _tag="PA4296"
rotein name confidence: Class 3 (function presence of conserved amino acid motif,
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                              proposed
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LGDLLGLSAGEVNSMSQLDTAINALDLIMAVAQVANKNSAVAVNLGIPGLANARLTVV
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complement (2640. . 2924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MHERILFGVLLLLSGTAWAADTPAVRPAAPATAEPQTATRAWLA IQASGRAASPVRQSATAAERQRAYQRYLKSYEHEIPEYLLEDRGFGESKN" complement (2947. .3684) /locus_tag="PA4299" complement (2947. .3684) /locus_tag="PA4299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Protein name confidence: Class previously reported genes of unknown i
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/note="Protein name confidence: Class previously reported genes of unknown similarity to any previously reported
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                                                                                                                                                                                                                                        /translation="MKALIGIGLCAALLGGCAALPGRDGPRECSQQLGQEQELQMNMV RDMIREGRLHAALANLESMPPGLLDVREERALILRRIGDPRARAEYQALLETCKAPEA HHGLGLLALRNGDSARAVLELREAARLRPTESRFRNDLGVALLKRGDRVGARFEFITA LELQQGGKLPATNILGLLYLQGDREDAQRLIERLQLDARDIRAAEARARSWGAVPTPG
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previously reported genes of unknown i
similarity to any previously reported
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protein_id="AAG07686.1"
                                                                                                                                                           locus_tag="PA4300"
                                                                                                nent (3681. .4592)
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           ss 4 (homologs of function, or no d sequences)"
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CDS

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RESULT 25
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  ACCESSION
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Best Local
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                                                                                                                                                                                                                               61;
AP005046 301925 bp DN Streptomyces avermitilis genomic DNA, 26/30.
AP005046 BA000030
                                                                                                                                                                                                                                           Similarity
                                                                                                                GGACCTGCCCGGCGAGGGCCTGCGGCACTACGATCCGGG
                                                                                                                                           CGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCG 135
                                                                                                                                                                                                 GCTGCTGATGATCGTCACCCCGCACCTGGTCCAGCCGCTGGCCGACGCACAGTTGCC 8051
                                                                                                                                                                                                                               Conservative
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complement (6745. .7929)
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complement (6745. .7929)
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MEMLVGLTGNRLPEQTLRLMICAALDVVVQITRLASGRRCISEVLEVLEVRDGVYVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 based on presence of conserved amino acid motif, structural feature or limited sequence similarity experimentally studied gene)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: hvbA"

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complement (4602...5486)
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LFVLLVLLVKLLRAESEASYAVPLLFAAGIGFLLPKQVLKHFAKARRALIADEMILFV
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Pred. No. 4.2e+02;
); Mismatches 38;
                                          DNA
                            complete
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                                                                                                                                                                                                                                                       Length 10348;
                          genome,
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E 3 (bases 1 to 301925)

Somura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kushida, N., Director-General of Biotechnology Center, Shiba, T., Sakaki, Y. and Hattori, M.

Direct Submission

Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)

This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hisashi Kikuchi(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Following url is also available. http://avermitilis.ls.kitasato-u.ac.jp Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikeda, H., Ishikawa, J., Hanamoto, A., Shinc Shiba, T., Sakaki, Y., Hattori, M. and Omura Complete genome sequence and comparative microorganism Streptomyces avermitilis Nat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Final finishing process and all annotation were done by H. Iked: and J. Ishikawa.
*1 Kitasato Institute for Life Sciences, Kitasato University
*2 National Institute of Infectious Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M. Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis MA-4680
Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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*4 National Institute of Technology and Evaluat

*5 School of Science, Kitasato University

*6 Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN, Genomic Sciences Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and all annotation were done by H. Ikeda
                                                                                                                                                                                                            1 protein"
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                                                                  ALDSGGREYGLRVALSFGAGVAVAQALNHARWYGLHTHWYWLPATAVFLVKPDLGPLA
SRVLCRAAGTVLGAVLFAGLAALLPRPEGLVALVVISGALIPVATRHFAAQTAVVTVL
VLALVMVGGEPQASWNRIGETALACAIVLLVGHLPTPGQRGGGVRARLARAHDAAHAY
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 LAHVLSGSGDRTGRWVLRREAYRALAEARAAIDLAAAELPALARHTEGTEEVAAVLER
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transl_table=11
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                  Streptomyces avermitili: 26/30.
AP005046 BA000030
AP005046.1 GI:29609904
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ilarity 59.1%;
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Streptomyces avermitilis MA-4680

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)

This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).

Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
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Shinose,M., '
Kikuchi,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Following url is also available.
http://avermitilis.ls.kitasato-u.ac.jp.
Location/Qualifiers
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Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
Kushida,N., Director-General of Biotechnology Center, Shiba,T.,
Sakaki,Y. and Hattori,M.
Direct Submission
Submitted (29-MAR-2002) Director-General of Biotechnology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S. Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis Mat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M. Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
*4 National Institute of Technology and Evaluation
*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
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chnology, Indian Delhi, Delhi

Harbor Laboratory,

11 BAC clone

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RESULT 27
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                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                             KEYWORDS
                                                                                                                                                                                     ACCESSION
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Best Local Similarity
                                                                           ORGANISM
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                               AC134925 DNA Oryza sativa (japonica cultivar-group) OSJNBa0041J17, complete sequence.
AC134925
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                                                                                                                                                         AC134925.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCGAGTCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCG
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Pred. No. 2.4e+02;
0; Mismatches 45
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                                                                                                                                                                                                                                         chromosome
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                                                                                                                                                                                                                                                                 linear
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4 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K.,
Ghazi, I.A., Yadav, M., Dixit, R., McCombie, W.R., Spiegel, L., de la
Pal, A.K., Dalal, V., Batra, K., McCombie, W.R., Spiegel, L., de la
Bastide, M., Zutavern, T., Muller, S., Nascimento, L., Balija, V.,
Bastide, M., Miller, B., Katzenberger, F., Andrade, M.V., Dike, S.,
Co'Shaugnessy, A., Palmer, L., Gaikwad, K., Sharma, T.R., Mohapatra, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase III by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSJNBa0041J17 overlaps clone OSJNBa0007D07 from base 100381 to base 148829. The overlap is from base 1 to base 48448 on OSJNBa0007D07.
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Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., *de la Pal, A.K., Dalal, V., Batra, K., *McCombie, W.R., *Spiegel, L., *de la Bastide, M., *Zutavern, T., *Muller, S., *Nascimento, L., *Balija, V., *Bell, M., *Miller, B., *Katzenberger, F., *Andrade, M.V., *Dike, S., *O'Shaughnessy, A., *Palmer, L., Gaikwad, K., Sharma, T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Singh, N.K.

Direct Submission
Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India
On Mar 21, 2004 this sequence version replaced gi:28604232.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-FEB-2003) IIRGS, NRC on Agricultural Research Institute, LBS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain, S.C., Batra, K., Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pal, A.K., Dalal, V., Singh, A., Sharma, T.R., Mohapatra, T. and Singh, N.K.
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Submitted (02-OCT-2002) IIRGS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain, S.C., Batra, K., Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pal, A.K., Dalal, V., Saikwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.
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Oryza sativa (japonica cultivar-group) chromosome OSJNBa0041J17, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
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                                                                                                       34119. .34200
/note="The assembly is covered by high qu
~~~~~rated from a transposed plasmid subc!
            /note="The assembly is covered by
derived from a transposed plasmid
68165. .69015
                                                                                          generated from a transposed 66330. .66375
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                                                                                                                                                                                                                                                                                /clone_,
                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                         clone="OSJNBa0041J17"
clone_lib="HindIII"
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                                                                       148829 bp DNA Oryza sativa (japonica cultivar-group) OSJNBa0041J17, complete sequence. AC134925
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                                                       AC134925.4
     Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="The assembly shows one A at this position. differs from the overlapping sequence of clone OSJNBa0007D07 (AC136481) which shows two As."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="The assembly is covered by
derived from a transposed plasmid
83360. .83610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="The assembly shows one T at this position. differs from the sequence of the overlapping clone OSJNBa0007D07 (AC136481) which shows two Ts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="The assembly shows at G at this position. 'differs from the sequence of the overlapping clone OSJNBa0007D07 (AC136481) in which the G is absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="The assembly shows one additional A compared to the sequence of the overlapping clone OSJNBa0007D07 (AC136481)."
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/note="The assembly is covered by high quality
derived from a transposed plasmid subclone."
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/note="The assembly is covered by high quality sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived from two transposed
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/note="The assembly is covered by high quality derived from a transposed plasmid subclone."
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derived from a PCR product."
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                                                         GI:45598398
   (japonica cultivar-group)
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Pred. No.
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REMARK
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase III by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSJNBa0007117 overlaps clone OSJNBa0007D07 from base 100381 to base 148829. The overlap is from base 1 to base 48448 on OSJNBa0007D07.
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Submitted (02-OCT-2002) IIRGS, NRC on
Submitted (08-OCT-2002) IIRGS, NRC on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K.,
Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K.,
Pal, A.K., Dalal, V., Batra, K., *McCombie, W.R., *Spiegel, L., *de la
Bastide, M., *Zutavern, T., *Muller, S., *Nascimento, L., *Balija, V.,
*Bell, M., *Miller, B., *Katzenberger, F., *Andrade, M.V., *Dike, S.,
*O'Shaughnessy, A., *Palmer, L., Gaikwad, K., Sharma, T.R.,
Mohapatra, T. and Singh, N.K.
Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone
OSJNB10141317, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-MAR-2004) IIRGS, NRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., Pal, A.K., Dalal, V., Batra, K., McCombie, W.R., Spiegel, L., de la Bastide, M., Zutavern, T., Muller, S., Nascimento, L., Balija, V., Bell, M., Miller, B., Katzenberger, F., Andrade, M.V., Dike, S., O'Shaugnessy, A., Palmer, L., Gaikwad, K., Sharma, T.R., Mohapatra and Singh, N.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 148829)
Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pa Gaikwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.
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Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pa Gaikwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.
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Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
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1 Bungtown Road, Cold Spring Harbor,
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 34119. .34200 /note="The assembly is covered by high generated from a transposed plasmid sub 66330. .66375
                                                                                                                                                       derived from
                                                                                                                                                                                                                                                                            organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
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                                                                                                note="The assembly is covered lerived from a PCR product."
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                                                                                                                                                                                                                                                                                                                                 (japonica
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                       igh quality sequences subclone."
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                                                                                                                              quality sequences
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Pal,A.K., Dalal,V.,
N.K.
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Mohapatra, T

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ACCESSION VERSION KEYWORDS

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/note="The assembly is covered by high quality derived from two transposed plasmid subclones." 69766. .69895
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/note="The assembly is
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79975. .
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/note="The assembly is covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="The assembly shows one A at this position. differs from the overlapping sequence of clone OSJNBa0007D07 (AC136481) which shows two As."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="The assembly shows at G at this position. differs from the sequence of the overlapping clone OSJNBa0007D07 (AC136481) in which the G is absent.
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RESULT 29
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Query Match Best Local S Matches 79

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Accession

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Direct Submission
Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas genome consortium, the DOE Joint Genome Institute, Production genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 349315)
Larimer, F.W., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S., Do Land, M.L., Pelletier, D.A., Beatty, J.T., Lang, A.S., Tabita, F.R., Gibson, J.L., Hanson, T.E., Bobst, C., Torres, J.L., Peres, C., Harrison, F.H., Gibson, J. and Harwood, C.S.
Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris
Nat. Biotechnol. 22 (1), 55-61 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genomes.
Rhodopseudomonas palustris CGA009
Rhodopseudomonas palustris CGA009
Rhodopseudomonas palustris CGA009
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
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Rhodopseudomonas palustris CGA009
BX572593 BX571963
BX572593.1 GI:39652705
                                                                                                                                                                                                                                  larimerfw@ornl.gov
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STISSERGRAVKLALSAGKLVLSVTNPDSGSATEELEVEYASDPLDIGFNSRYLLDIA
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Direct Submission
Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 349315)
Larimer, F.W., Chain, P., Hauser, L., Lamerdin, J., Malfatti Land, M.L., Pelletier, D.A., Beatty, J.T., Lang, A.S., Tabit Gibson, J.L., Hanson, T.E., Bobst, C., Torres, J.L., Peres, C Harrison, F.H., Gibson, J. and Harwood, C.S.
Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris Nat. Biotechnol. 22 (1), 55-61 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete genomes.
Rhodopseudomonas palustris CGA009
Rhodopseudomonas palustris CGA009
Bacteria; Proteobacteria; Alphaproteobacteria; Rh
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Larimer, F.W. and Harwo
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Rhodopseudomonas palustris
BX572593 BX571963
BX572593.1 GI:39652705
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tris CGA009
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., Tabita,F.R.,
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kawai, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from ianonica rice
E 2 (bases 1 to 674)

S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Oka, M., Ooka, H.,
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Oryza sativa (japonica cultivar-group)
Cryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Pred. No. 4.3e+02;
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                               VERSION
KEYWORDS
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AK063727/c
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                                                                                                                                        DEFINITION
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AKU63727.1 GI:3237.1
FLI_CDNA; oligo-capping
FLI_cDNA; oligo-capping
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Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute or Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute or Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

Tel:81-29-838-7007, Fax:81-29-838-7007)
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                                                                                                                                                             Oryza sativa (japonica cultivar-group) cDNA clone insert sequence.
                                                                                                                                  AK063727
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-120-E01"
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58.2%;
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:001-120-E01, full
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Yamada,H., Ya
Yoshimura,A.
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Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 105-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 105-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, 105-838-7007, Fax:81-29-838-7007)

Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
                                                                                                                                                                                                                                                                                                                                                                                                URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
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Science 301 (5631),
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Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
                                                        Direct Submission.
Submitted (04-OCT-2003) The In
Medical Center Dr, Rockville,
(hases 1 to 133449)
                                                                                                                                                                           Buell,R.
Direct Submission
Submitted (28-SEP-2002) The In
Medical Center Dr., Rockville,
4 (bases 1 to 133449)
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1 (bases 1 to 133449)

1 (bases 1 to 133449)

Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M., Overton II,L.L., Tsitrin,T., Kim,M.M., Bera,J.J., Jin,S.S., Fadrosh,D.W., Tallon,L.J., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.S., Riedmuller,S.B., Utterback,T.T., Feldblyum,T.V., Yang,Q.Q., Haas,B.J., Suh,B.B., Peterson,J.J., Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M.
Oryza sativa chromosome 3 BAC OSJNBb0106M04 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence. AC107207
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Direct Submission
Submitted (16-JAN-2002)
Medical Center Dr, Rocky
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                      Submission
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/db_xref="taxon:39947"
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e, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical Center Dr, Rockville, MD 20850, USA, r
On Oct 4, 2003 this sequence version replaced
Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This BAC overlaps with rice BAC OSJNBa0079B15 (AC099043) OSJNBa0072F13 (AC133450).
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                                                                                                 /rpt_family="Oryza"
complement(4844. .4899)
/rpt_family="Oryza"
complement(4845. .4899)
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complement(4845. .4898)
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  /rpt_family="(TA)n"
complement(4846..4899)
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4843
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4843. .4901
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d gi:23343713.
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complement (20302. .21405)
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5722. .5742
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SRGFGFVEFADEAATLRALADDEMPNHVFRGRKVDVKRAERRHDHKQTSPSIKNQNDS SRGFGFVEFADEAATLRALADDEMPNHVFRGRKVDVWANRTTTNRARGFGFISF VQKNQFIFQKKVFVGGLHETVTVKDLISYFEKFGTITDAVVMRNRTTNRARGFGFISF VGKNQFIFQKVFVGGLHETVTVKDLISYFEKFGTITDAVVMRNMDMSLSPITYYDGMV HVHPYTPYTFGCVTPLAHLTHSGYGYGGPIDYSCYAYGGPIGHQHDLVGSYYYYAKDYS
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                                  /translation="MDSRLVAFSHRRRRWILLAAGGAAAVFGAYKIYHHPAVAARRRRLARLAAGAVAAFLDAAAASADAAALVASDLSDFVRSGSDELPRSVTQLAKLAASPEVSATVSAISEAITAGILRGVGSDSGPGSGGGVALSDRLVDRLFSESGERLAAAIAGSFARHLVAAIYSASSTPGETSSPMKWVNLIATGKGQXAISNWVEVFVSTAVGVFVDKTIHINTYVAAIYSASSTPGETSSPMKWVNLIATGKGQXAISNWVEVFVSTAVGVFVDKTIHINTYVAAIYSASSTPGETSSPMKWVNLIATGKGQXAISNWVEVFVSTAVGSGSNGAGEG
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complement(10905. .11360)
/gene="OSJNBb0106M04.3"
/note="contains Pfam prof
  YDQLFQGLTNASHDAKVKELLVSVCNGAVETMVKATHHVMSNANYKSVGSGSNGAGEG
WVETVSSTLAVPSNRKFVLDVTGRVTFETVRSFLEFALWKMHAGAKKGGNTVMDSGLR
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18697. .18724
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|1202. .11238
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/protein_id="AAR87318.1"
/db_xref="GI:40539061"
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                                                                                                                                                                                                                      product="expressed protein"
protein_id="AAR87321.1"
/db_xref="GI:40539064"
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L6238. .16258
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SM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 133449)
S Huell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,
Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,
Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,
Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V.,
Yang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J.,
White, O., Salzberg, S.L. and Fraser, C.M.
Oryza sativa chromosome 3 BAC OSJNBb0106M04 genomic sequence
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Direct Submission
Submitted (01-JAN-2004) The Institute for Genomic Research, Submitted (01-JAN-2004) The Institute for Genomi
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Submitted (16-JAN-2002) The Institute for Genomic Research,
Submitted (Price Dr. Rockville, MD 20850, USA
3 (bases 1 to 133449)
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Medical Center Dr, Rock
(bases 1 to 133449)
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Oryza sativa chromosome 3 BAC OSJNBb0106M04
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llarity 58.2%;
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22556. .22728
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21205. .21286
/rpt_family="(CGG)n"
21330. .21352
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22859. .22954
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                                                                                                                                                                                                                                                                                                                                                                                                     -2002) The Ir
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e, MD 20850, USA
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http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
OSUNBa0072F13 (AC133450).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of several prediction programs including Fgenesh (http://www genscan and Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM
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                                                                                  BAC
                                                                            overlaps with rice BAC
                                                                            OSJNBa0079B15
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                                                                                  099043) and
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.softberry.com/),
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FEATURES repeat_region repeat_region CDS mRNA repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region source /rpt_family="Oryza"
complement(4845. .4899)
/rpt_family="Oryza"
complement(4845. .4898)
/rpt_family="Oryza"
4845. .4897 complement (4846.....4899)
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complement (4848...4897)
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gene
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WVETVSSTLAVPSNRKFVLDVTGRVTFETVRSFLEFALWKMHAGAKKGGNTVMDSGLR
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complement (10905. .11360)

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NCE 1 (bases 1 to 150743)

DRS Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Yang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.

Oryza sativa chromosome 3 BAC OSJNBa0072F12 ~~
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                             Direct Submission
Submitted (31-JUL-2004) The Institute for Genomic Submitted (31-JUL-2004) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA, rbuel On Mar 31, 2004 this sequence version replaced gi:
                                                                                                                                              Submitted (31-MAR-2004) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA 5 (bases 1 to 150743)
                                                                                                                                                                                                                                    Direct Submission
Submitted (16-OCT-2003) The In
Medical Center Dr. Rockville,
4 (bases 1 to 150743)
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Submitted (12-SEP-2002) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150743)
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                                                                                                                                   Buell, R
                                                                                                                                                                                                    Direct Submission
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AC133450
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clone OSJNBa0072F13 is from orientation of the sequence
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                                                   correspondence to:rice@tigr.
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e 3 BAC OSJNBa0072F13 genomi
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 Oryza sativa chronis from SP6 to T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This BAC overlaps with rice BAC OSJNBb0106M04 (AC107207) and
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complement(join(3737. .4313,4877. .5250,7227. .7443,
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LLRAHRRGFRRRRGERGYAGWWGPSTSSRPSGLRAAGVVEFLRRLSTKEVRVRSSLAA

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DAMENUHAAIAVAGLGHIKVTTSISQATIGIHIPPSASEFTDEAKSSFLSYVIPFLEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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THAPLLANLYPYFIYSYNPGGMDISFALFTASER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3737. .8420)
/gene="OSJNBa0072F13.1"
/note="contains Pfam profile PF00332: Glycosyl hydrolases
                                                                                                                                                                                                                                                                                                                                                              SGWPQAGERAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join (<3737. .4313, 4877. .5250, 7227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="japonica cultivar-group"
789. .2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="OSJNBa0072F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .150743
                                                                                                                                                                                                                                                                                                   _family="(CGG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family="(CCCG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AC092781)
                                                                                                                                                                                                                                                                                                                                      .6698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y="T-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (japonica cultivar-group)"
                                      repeat_region
                                                                                            repeat_region
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                                                                                                                                                                                                                                           / Dr. Lumity - (1974)
/ Complement (21609. .24979)
/ gene="OSJNBa0072F13.4"
/ note="predicted by fgenesh"
complement (join(<21609. .22157,23140. .23202,24095. .24156,
24718. .>24979))
/ gene="OSJNBa0072F13.4"
complement (join(21609. .22157,23140. .23202,24095. .24156,
24718. .24979))
/ gene="OSJNBa0072F13.4"
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/ product="hypothetical protein"
/ protein_id="AAT85044.1"
/ db_xref="GI:50872444"
/ translation="MSSSFSFPSSSFIPSSLSLILSLSPGLSLRWGAAAAVAAGGGGG
/ translation="MSSSFSFPSSSFIPSSLSLILLSLSPGLSLRWGAAAAVAAGGGGG
                                         /rpt
24911
                                                                                               24815
                                                                                                                  PLIMSPAWGVAEEDAATGDELRRGTWMAEDVAAPATISGVDI
GITGDDLRRGSWRMPPPATSSGTIRGQWDHRRRF"
                                                                                                                                            GGRERQRRRRRYMGELKRALDARCHMILEMPTGTGKTAASSSPYKRHVDDTLDEDRST
PPRGRHKKLATCRTKQIGAIFMYANSEVLKCYTTGYTVPSAWDGIASSCTISLSHVFS
ACVTAADDSFMVAVIACSSLPPVTAPMRTLDDDVGMWTVEDAASATSSGMRHGWWRTR
PLTMSPAWGVAEEDAATGDELRRGTWMAEDVAAPATISGVDRGGCRCRRQALARDVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="knotted1-type homeobox protein"
/protein_id="AAT85041.1"
/db_xref="GI:50872441"
/translation="MESFASLAGGGSSSTTARLPELISPEN
/tsaslation="MESFASLAGGGSSSTTARLPELISPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="OSJNBa0072F13.3"
/note="nearly identical to knotted1 type
/note="nearly identical to knotted1 type
OSH43 GB:BAA79225 1 GI:5103727 (Oryza sat
expression of the rice KN1 type homeobox
during embryo, shoot, and flower developm
(9), 1651 1664 (1999)); contains Pfam pro
KNOX1 domain and PF03791; KNOX2 domain; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YREELERPILEAAEFFSRVETQLDSLAGTGSSEEEQDPSDK
RQVFSKRTKKGKLPKEARQKLLHWWELHYKWPYPSEMEKMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from this gene"

complement(join(14329...14836,14939...151.
19127...19264,19398...19852))
/gene="OSJNBa0072F13.3"

complement(join(14585...14836,14939...151.
19127...19264,19398...19712))
/gene="OSJNBa0072F13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
complement(14329. .19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKKVGAPPDVLTKLTAVPAAQQLDEADGHPRRRHEPQRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6530. .16560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
11920. .11968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VATSSALASSARWRERVEKAAAAVAAGEGDEGDGAGARGR
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10072. .10542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MEHVPLLGDAFLSAPCQLFVGSRCVGGLGRSWTRLLHLRFPLLPSLGGGRRRWGGTRGGCEREKEATVTAMTAPLSPPLEAPVLATEDHEDDVVVVVAAAATSSALASSARWRERVEKAAAAVAAGEGDEGDGAGARGREREGKDGDGAERRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )RKRHWKPTPVAGTAFPTMEAAGGGFRHSGHGGGLAAAAALPLYMGRPFVVDGMYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAT85039.
db_xref="GI:50872439"
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product="hypo
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                                         family="(CCG)n"
[. .24971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="(CAG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="AT_rich"
                                                                                            .24883
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d="AAT85039.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENPDHISPPPLLYQLLAGP
CAEIMSHPQYSALLAAYLG
DDPDQLDQFMDAYCSMLTR
KQLKHQLLRKYGGSLGDL
TTLAQTTGLDQKQINNWFI
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AC133450/c
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AUTHORS
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TITLE
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Best Local
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mes 64; Conservative
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                                                                                                                                                                                                                                                                  Direct Submission
Submitted (31-MAR-2004) The Institute for Genomic Submitted Center Dr, Rockville, MD 20850, USA (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 150743)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,
Overton II, L.L., Tsitrin, T., Kim, M.M., Bera, J.J., Jin, S.S.,
Fadrosh, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S.,
Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblym, T.V.,
Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblym, T.V.,
Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblym, T.V.,
clone.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (http://www.softberry.com/),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-SEP-2002) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150743)
                                                                                                                                              Submitted (31-JUL-2004) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Mar 31, 2004 this sequence version replaced gi:37693579. Address all correspondence to:rice@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-OCT-2003) The In
Medical Center Dr, Rockville,
4 (bases 1 to 150743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang,Q.Q., Haas,B.J., Suh,B.B., Peterson,J.J., White,O., Salzberg,S.L. and Fraser,C.M. Oryza sativa chromosome 3 BAC OSJNBa0072F13 genunchished
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Oryza sativa chromosome 3 BAC
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                                                                                                                                                                                                                                                           Buell, R.
                                                                                                                                                                                                                                                                                                                                                                      Buell, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buell, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buell, R.
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                                                                              clone OSJNBa0072F13 is from orientation of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bases 1 to 150743)
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/note="nearly identical to P type R2R3 Myb protein
/note="nearly identical to P type R2R3 Myb protein
GB:AAQ54875 1 GI:33773103 (Sorghum bicolor), Ordered
origin of the typical two and three repeat Myb genes
(Gene 326, 13 22 (2004)); contains Pfam profile PF00249:
Myb like DNA binding domain; EST cDNA AK112018 from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene"
join(30040.
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                                                                                                                                                                                                                                                                                                                                                                                                             Institute for G
e, MD 20850, USA
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C OSJNBa0072F13 genomic sequence
                                                                              Oryza sativa
is from SP6 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research,
                                                                                                                                                                                                                                                                                                                         Research,
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CDS mRNA

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gene

repeat_region repeat_region

_family="AT_rich"

family="AT_rich"

repeat_region

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FEATURES
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                                                                       repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats a identified by repeatmasker (Arian Smit,http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC overlaps with rice BAC Bb0094003 (AC092781).
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/rpt_family="(CGG)n"
8946. .8991
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                                                                                                                                                                                                                                                                                                                                       complement(join(<3737. .4313,4877.
8374. .$4420))
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complement(join(3737. .4313,4877.
8374. .8420))</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="T-rich" 3736. .3860
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                                                                                                                                  LGGTGIRVVGGAPNYDLPALAHGGTAATAAWIQAYPMMLFRFVIVGNEVAGADTQLLV
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3580.
                                                                                                                                                                                                                                             /product="putative Glycosyl hydrolases
/protein_id="AAT85038.1"
/db_xref="GI:50872438"
                                                                                                                                                                                                                                                                                                                                                                                                                                      family 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt family="(CCCG)n"
complement(3737. .8420)
/gene="OSJNBa0072F13.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                       gene="OSJNBa0072F13.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="japonica cultivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  map="R2443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="OSJNBa0072F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                  .4313,4877.
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                                                                                                                                                                                                                                                                                   family 17 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (14329. .14836,14939. .15135,18892. .19000, 19127. .19264,19398. .19852))
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GS"

16530. .16560
                                                                                                                                                                                                                                                                                                                                                                                     complement(21609..24979)
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complement(join(<21609..22157,23140..24718..>24979))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt family="AT rich"
complement(14329. .19852)
/gene="OSJNBa0072F13.3"
/note="nearly identical to knotted1 type homeobox protein
/note="nearly identical to knotted1 type homeobox protein
OSH43 GB:BAA79225 1 GI:5103727 (Oryza sativa), Regional
expression of the rice KN1 type homeobox gene family
during embryo, shoot, and flower development(Plant Cell 11
(9), 1651 1664 (1999)); contains Pfam profile PF03790:
KNOX1 domain and PF03791: KNOX2 domain; EST cDNA AK107296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MEHVPLLGDAFLSAPCQLFVGSRCVGGLGRSWTRLLHLRFPLLPSTSSLGGGRRRWGGTRGGCEREKEATVTAMTAPLSPPLEAPVLATEDHEDDVVVVVAAVATSSALASSARWRERVEKAAAAVAAGEGDEGDGAGARGREREGKDGDGAERRE"
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11992.
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19984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0435.
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                                                                                                                                                 GITGDDLRRGSWRMPPPATSSGTIRGQWDHRRRF'
                                                                                                                                                                                                                                                                                                                                                                    gene="OSJNBa0072F13.4"
gene="OSJNBa0072F13.5"
note="nearly identical
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12119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="AT_rich"
4. .20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="(CAG)n"
                                                             family="GA-rich"
                                                                                                          family="(CCG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .10560
 identical
 to P type R2R3 Myb protein
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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AY081837
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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
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2 (bassa
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Bradyrhizobium japonicum isolate ppM200p9-2 putati (amiC) gene, partial cds; pyruvate dehydrogenase (2-dehydro-3-deoxyphosphogalactonate aldolase (dgoA 2-dehydro-3-deoxygalactonate kinase (dgoK), putati monooxygenase (luxA2), HpaC (hpaC), and sigma 54 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes, co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mueller, P.
ThKPK2 insertions in the (pyruvate dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (04-MAR-2002) Biology, Cell Biology and Submitted (04-MAR-2002) Biology, Karl-von-Frisch-Str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY081837.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soybean nodules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACCAGCTCCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bases 1 to 8973)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete cds; and
                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 5.5e+02;
0; Mismatches 46;
conserved hypothetical
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activator (acoR)
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eraction within
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Marburg 35032,
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complement (5383. .6288)
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  ACCESSION
VERSION
KEYWORDS
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AY081837/c
LOCUS
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gene

gene

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Bradyrhizobium japonicum isolate pPM200P9-2 putative amidase (amiC) gene, partial cds; pyruvate dehydrogenase (poxB), 2-dehydro-3-deoxyphosphogalactonate aldolase (dgoA), 2-dehydro-3-deoxygalactonate kinase (dgoK), putative alkanal monooxygenase (luxA2), HpaC (hpaC), and sigma 54 activator (genes, complete cds; and unknown genes. AY081837.1 GI:20257158
                                                                                                                                                                                                                                                                                                                                                                                                                             GATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGGAGCTGGTCATCGCTCATCGTCGAGTCGGCGGCCGCCGACT
                                                                                                                                                                                                                                                                                                                                                                           GATCGCGACCAGCGGACGCTTCATCGACGGAAAGGGA 5359
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7615. .8229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMFDFLKPHIKPLQAPHPPNRVAGLSKNSDTLKLAGERGFIPMSLNLNPAYVGSHWDS
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Pred. No. 1e
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REFERENCE
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ORGANISM
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Submitted (04-MAR-2002) Biology, Cell Biology and Applied B
Submitted (04-MAR-2002) Biology, Cell Biology and Applied B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Three insertions in the (pyruvate dehydrogenase) soybean nodules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Germany
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Bacteria; Proteobacteria; Alphaproteobacteria;
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                                       'gene="poxB"
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7615. .8229
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'gene≈"dgoA"
'no+~~"
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Direct Submission

Submitted (03-AUG-1999) Production Sequencing Se
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AC008771
AC008771.4 GI:13162500
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                                                                                                                                                                                                                                                                                                                                                                                          www.jgi.doe.gov
Finishing Completed at
www-shgc.stanford.edu
Quality: Phrap Quality
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DOE Joint Genome Institute and Stanford Human Genome Center
Direct Submission
One Joint Genome Institute, 2800 Mi
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Mammalia; Eutheria; Primates; C
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/transl_table=1
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complement (8407. .8973)
                                                                                                                                                                            Location/Qualifiers
1. .123169
                                                                                                                 organism="Homo sapiens"
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/protein_id="AAM12344.1"
/db_xref="GI:20257159"
                                                      /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 1e+03;
0; Mismatches 38
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Catarrhini; Hominidae;
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Local Similarity 55.0%;
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Submitted (03-AUG-1999) Production Sequencing Facility, DOB (
Submitted (03-AUG-1999) Production Sequencing Facility, DOB (
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598
3 (bases 1 to 123169)
DOB Joint Genome Institute and Stanford Human Genome Center.
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AC008771
AC008771.4 GI:13162500
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DOE Joint Genome Institute.
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1 (bases 1 to 123169)

DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-17790 G24283.
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SHGC-84992 G53847
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2015H6"
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                                                                                                                         <u>,</u>
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Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
NOTE: Bacterial transposon excised at 89327.
Location/Qualifiers
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Submitted (30-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
6 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
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Submitted (09-NOV-2000) DOE Joint Genome Institute, 2
Submitted (09-NOV-2000) DOE Joint Genome Institute, 2
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome
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Homo sapiens chromosome 5 clone CTD-2327L5, complete sequence.
AC018764
AC018764.8 GI:28933541
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On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 126052)

DOE Joint Genome Institute and Stanford Human Genome Center.
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CGAGTCGGCCGCCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGA 126
                                                                         GAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCTCATCGT
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Joint Genome Institute.
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llarity 55.0%;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 6.2e+02;
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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RESULT 1 US-09-434-288-7

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; TYPE: DNA ; ORGANISM: Streptomyces narbonensis US-09-434-288-7
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; ORGANISM: Streptomyces narbonensis
US-09-434-288-7
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; Patent No. 6303767
; GENERAL INFORMATION:
; APPLICANT: Betlach (
    APPLICANT: McDaniel)
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APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
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PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA TITLE OF INVENTION: CONSTRUCTS THEREFOR FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
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Patent No. 6294328

GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                 Query Match 22.1
Best Local Similarity 59.2
Matches 58; Conservative
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Best Local Similarity 59.2

Best Local Similarity 59.2
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                                                                                                                                                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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ORGANISM: Mycobacterium tuberculosis
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SOFTWARE: SEQ ID NO 7

ENGTH:

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Query Match

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US-09-103-840A-1; Sequence 1, Application  
; Patent No. 6294328;
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APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Best Local
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LENGTH: 4411529
TYPE: DNA
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAITILE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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SOFTWARE: PatentIn Vei
                                                                                                                                                            TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                   ENGTH: 4411529
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                                                                       Local Similarity 59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGCCAGTCGGTGGCGTGGTGATCATCTTCAACCGC
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 GCGGTTGAAGATGATCACCACGCCCACCGACTGGCCGCGATACGGCGGCTACGCGCTGGC 4259576
                                     CCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCG
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Pred. No. 10;
0; Mismatches
                                                                                        Pred. No. 10;
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                                                                        Mismatches
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US-09-252-991A-4417/c
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US-09-252-991A-4417
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAP
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 4417
LENGTH: 747
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SEQ ID NO 4417
LENGTH: 747
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                                                                                                                      Matches
                                                                                                                                                  Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAP
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                     Local
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                                                                                                                                    Similarity
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TGAGCGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAGCGAGAT
                                                   ACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGAC 122
                                                                                   GICGGCGGCCGGAGCTGGTCAICTCGCTCAICGTCGAGTCGGCGGCCGCCGACTCGACGA 92
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JMBER: US 60/094,190
1998-07-27
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57.0%;
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0; Mismatches
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                      139
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                                                                                                                        Query Match
Best Local S
Matches 61
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US-09-252-991A-4622
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APPLICANT: Marc J. R.
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4622, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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LENGTH: 3225
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ENGTH: 3225
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                                                                                                                    h 21.7%;
Similarity 57.0%;
61; Conservative
GCTGCGCCACCGCCGTCGCCGGCCTCCTGCCAGATGTCCATCAT
                          TGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGAT 139
                                                        CATCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCG
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BER: US 60/074,788
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                                                                                                                  Score 33.4; D: Pred. No. 11; 0; Mismatches
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Pred. No. 11;
0; Mismatches
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AND AMINO ACID SEQUENCES RELATING
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RESULT 12
US-09-513-999C-8640/c
; Sequence 8640, Application US/09513999C
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US-09-513-999C-8640
                                                                     GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards,

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.
                                   TITLE OF INVENTION: Expressed Sequence Tags and Encoded Humanett No. 6783961
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID: 08640
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2000-C
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APPLICANT: Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 345
OTHER INFORMATION: m=a
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OTHER INFORMATION: k=g
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OTHER INFORMATION: y=c
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OTHER INFORMATION: y=c
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LOCATION:
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NAME/KEY: misc_feature
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OTHER INFORMATION: k=g
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NAME/KEY: misc_feature
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                               246 GCCCGACGTGGTCATT
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APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 2360

LENGTH: 1110

TYPE: DNB
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; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8640
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local S
Matches 48
Query Match
Best Local Similarity 60...
54; Conservative
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NAME/KEY: misc_feature
LOCATION: 345
OTHER INFORMATION: m=a or c
-09-513-999C-8640
                                                                 TYPE: DNA
ORGANISM: Myxococcus
-09-902-540-2360
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NAME/KEY: misc_feature
TOTATION: 336
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: 320
OTHER INFORMATION: k=g
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OTHER INFORMATION: n=a,
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Similarity 62.3%;
48; Conservative
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             Score 32.4; D
Pred. No. 18;
0; Mismatches
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genom
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2360
LENGTH: 1110
TYPE: DNA
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US-07-841-651-1
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US-09-902-540-2360/c
; Sequence 2360, Application
; Patent No. 6833447
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ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,651
FILING DATE: 19920224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saraivar
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applic Patent No. 5410031
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Matches
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TITLE OF INVENTION: Cloning and
TITLE OF INVENTION: Mammalian Na
TITLE OF INVENTION: SGLT Family
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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54; Conserv
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California
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nilarity 60.0%;
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Pred. No. 18;
O; Mismatches
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                                                                                                             Version
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RESULT 16
US-07-841-651-1/c
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REFERENCE/DOCKET NUMBER: 8772
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-44000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07841651
Patent No. 5410031
GENERAL INFORMATION:
APPLICANT: Pajor, Ana M
                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,651
FILING DATE: 19920224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, SaraLynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 8772
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEPHONE: (818) 796-4000
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                 TELEFAX: (818) 795-6321 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wright, Ernest M
TITLE OF INVENTION: Cloning and Functional Expression of a
TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter:
TITLE OF INVENTION: SGLT Family
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STATE: California
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nes 51; Conserv
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LOCATION:
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2238 base pairs
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225 South Lake A
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RESULT 18
US-09-902-540-1100/c
; Sequence 1100, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Ge:
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1100

LENGTH: 15447
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; ORGANISM: Myxococcus xanthus
US-09-902-540-1100
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Best Local Similarity 62...
51; Conservative
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NAME/KEY:
LOCATION:
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MOLECULE TYPE: CDI
HYPOTHETICAL: NO
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ORIGINAL SO
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No. 6833447
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SM: Oryctolagus cuniculus
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Pred. No. 18;
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1100
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US-09-252-991A-8862/c
; Sequence 8862, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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US-09-252-991A-8862
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Best Local Similarity 57.4
58; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1100
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                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
            PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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Pred. No. 19;
0; Mismatches
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Pred. No. 2
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECTITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15671
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862
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                                                                                                                                                                                                                                                                                sequence 15671, Application US/09252991A
Patent No. 6551795
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 ORGANISM:
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                                  LENGTH: 807
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VENTION: NUCLEIC ACID AND AMINO ACID
VENTION: AERUGINOSA FOR DIAGNOSTICS I
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Pseudomonas aeruginosa
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nilarity 57.4%;
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RESULT 24
US-09-252-991A-8753/c
Commence 8753, Application US/09252991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 8753
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8753
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US-09-252-991A-8753
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Best Local Similarity
Matches 58; Conser
                                                                                                       NUMBER OF SEQ
SEQ ID NO 8753
 Query Match
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                                                                                                                                      CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1:
                                                   LENGTH: 876
TYPE: DNA
ORGANISM: Pseudomonas
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Pred. No. 20;
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Pred. No. 20;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15578
                                                                                                                            FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15578
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
US-09-252-991A-15578/c
                                                              ; ORGANISM: Pseudomonas US-09-252-991A-15578
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US-09-252-991A-15578
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US-09-252-991A-15578
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Patent No. 6551795
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              Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                 TYPE: DNA
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                                                                                                                 LENGTH:
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Conservative
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NUCLEIC ACID AND AMINO ACID
              20.9%;
57.4%;
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Score 32.2; D
Pred. No. 20;
0; Mismatches
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FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15737

LENGTH: 1869

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-15737
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US-09-252-991A-15737/c
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; ORGANISM: Pseudomonas
US-09-252-991A-15737
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US-09-252-991A-15737
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Best Local Similarity
Matches 58; Conserv
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SEQ ID NO 15737
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
                                                                         Matches
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15737, Ap
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Patent No. 6551795
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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42
                                                                       Similarity 58; Conser
CAGCCCGAGCTGCTCGCGGAAATCGGCGTCGCGTACCGCAGCGCAGTTGGCCGCGTAGCC 1193
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                                   CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT
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nilarity 57.4%;
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                                                                     Score 32.2; Di
Pred. No. 20;
0; Mismatches
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Pred. No. 20;
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                                                                                                         Length 1869;
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US-09-252-991A-8973/c
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US-09-252-991A-8973
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US-09-252-991A-8973
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LENGTH: 1899
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GENERAL INFORMATION:
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SEQ ID NO 8973
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APPLICANT: Marc J.
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                                                                                                                        Matches
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAP
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                      Local
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                                                                                                                     l Similarity
58; Conserv
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                                                    GGCATGATCTGCCCGTTGCCCTCGGCGCGTTGCGGCCGATGGTGAT
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Pred. No. 20;
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ATCGGCTTGCCGGCGCAGCAATACTCGTTGAGGGTCGGGGT 1779

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Secont Reference: 38-10(15849) B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10
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US-09-902-540-3748/c
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                                                                                                                                        Query Match
Best Local S
Matches 50
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                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3748
LENGTH: 921
TYPE: DNA
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3748
LENGTH: 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3748, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.8%;
Best Local Similarity 62.5%;
Matches 50; Conservative
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                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Myxococcus xanthus
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                                                                                                                                                       Local Similarity
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                                                                                                                                         50;
                                                             GGCGAGCACGCGGCTGCCGTCGGTCATCTCGCCCAGCTTCTGATTCACGGCGGACAGCGC
GGCGCCGGTGGAGATGCCCA
                                GACGATGAGCGAGATGACCA 107
                                                                                                GTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTC
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Pred. No. 22;
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Pred. No. 22;
782
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Sequence 7905, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 7905

LENGTH: 1093
                                                                                                                                                                                                                                            Sequence 7905, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

ITITLE OF INVENTION: Myxococcus xanthus Genome Seq

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

LENGTH: 1093

TYPE: DNA

ORGANISM: MYSOCOCCUS
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Best Local S
Matches 68
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US-09-902-540-7905
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Best Local Similarity
                                                                         408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
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                               61 CATCGTCGAGTCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAG
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                                                                                                                                                               Similarity
  CTCCGCCGCGACGACGCCTGCGCCAGCCCGGTGAGCTGACCGCTCAG
                                                                     CCGCGTCAGCTCGTCCGACAGCGCCGTGTGCAGGGCGAGGTGGGCGCG
                                                                                                  CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCATCTCGCT 60
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                                                                                                                                         20.8%; ilarity 53.1%; Conservative
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                               TCCGGCCGCCG 120
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US-09-032-372-6
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CLONE:
US-09-032-372-6
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APPLICANT: Lal, Preeti
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incvt^ "
                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pair
                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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GAGGAGGAGCGAGCCAAGCTGCAC 294
                        GACGATGAGCGAGATGACCAGCTC 148
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Hillman, Jennifer I
Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                       20.8%; ilarity 51.4%; Conservative
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RESULT 37
US-09-902-540-797
; Sequence 797, Application US/09902540
; Patent No. 6833447
GENERAL INFORMATION:
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US-09-032-372-6/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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MEDIUM TYPE: Diskett
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APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
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ADDRESSEE: Incyte Ph
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78191
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STRANDEDNESS:
TOPOLOGY: line
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REGISTRATION NUMBER: 30
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OPERATING SYSTEM:
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nucleic acid
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Hillman, Jennifer I
Corley, Neil C.
Guegler, Karl J.
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Pred. No.
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; ORGANISM: Myxococcus
US-09-902-540-797
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US-09-902-540-797/c
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; ORGANISM: Myxococcus xanthus
US-09-902-540-797
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SEQ ID NO 797
LENGTH: 7994
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Best Local Similarity
Matches 68; Conserv
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APPLICANT: Hinkle, C
APPLICANT: Slater, S
APPLICANT: Wiegand,
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LENGTH: 7994
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/90 CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences
FILE REFERENCE: 38-10(15849)B
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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ICANT: Slater, Steven C.
ICANT: Wiegand, Roger C.
ICANT: Wiegand, Roger C.
REFERENCE: 38-10(15849)B
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                              ACTCGACG
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Pred. No. 25;
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FILE REPERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1182
LENGTH: 17897
TYPE: DNA
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                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(17897)
OTHER INFORMATION: unsure
US-09-902-540-1182
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                                                           Query Match
Best Local S
Matches 50
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US-09-902-540-1182
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1182
LENGTH: 17897
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                       ORGANISM: Myxococcus xanthus
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NAME/KEY: unsure
LOCATION: (1)..(17897)
OTHER INFORMATION: unsure
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  GGCGAGCACGCGGCTGCCGTCGTCATCTCGCCCAGCTTCTGATTCAC
                            GTCGAGTCGGCGGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGC
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GGCGGACAGCGC 13409
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                           GCCGCCGACTC 87
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13526
LENGTH: 2496
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US-09-252-991A-13526/c
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US-09-252-991A-13526
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US-09-252-991A-13526
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Best Local S
Matches 49
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Best Local S
Matches 49
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13526
LENGTH: 2496
TYPE: DNA
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GENERAL INFORMATION:
                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
)9-252-991A-13526
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les 49; Conservat
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GGCCATCTGCGGCTGCAG 1013
                                   GACCAGCTCCGGCCGCCG 120
                                                                            GGAACAGATCCTGATCAGCACCGTCGGCGGCGCCGACGTCAAGCCGAAGAGCGAGAA 1031
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ilarity 62.8%;
Conservative
                                                                                                                                                          Conservative
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Pred. No. 29;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13933
LENGTH: 2622
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13933
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US-09-252-991A-13933
RESULT 45
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SEQ ID NO 13933
LENGTH: 2622
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Best Local
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Patent No. 6551795
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Best Local
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                CTGATCÁGGÁTCTGTŤCC
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ilarity 62.8%;
Conservative
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NUCLEIC ACID AND AMINO ACID
AERUGINOSA FOR DIAGNOSTICS A
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Pred. No. 29;
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Pred. No. 29;
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Sequence 13826, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13826
LENGTH: 2685
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13826
Search completed: April Job time : 154 secs
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                                                                                                                                                                            1576 GGAACAGATCCTGATCAGCACCGTCGGCGGCGCCGCCGACGTCAAGCCGAAGAGCGAGAA 1635
                                                                                                                                                                                                        43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
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                  9, 2005, 00:55:08
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